

FIG. 1

PROTEIN ALIGNMENT OF MOUSE, HUMAN AND RAT Nav1.3

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|-------------------|-------|-----------------------------------------------------|
| mNav1.3 wild-type | (1) | MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK |
| hNav1.3_NM_006922 | (1) | MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK |
| hNav1.3_AF225986 | (1) | MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK |
| rNav1.3_NM_013119 | (1) | MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDIDDENKPK |
| mNav1.3 wild-type | (51) | PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF |
| hNav1.3_NM_006922 | (51) | PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF |
| hNav1.3_AF225986 | (51) | PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF |
| rNav1.3_NM_013119 | (51) | PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYKKTFVANKGKAIF |
| mNav1.3 wild-type | (101) | RFSATSALYILTPINPVRKIAKILVHSLFSMLIMCTILTNCVFMTLSP |
| hNav1.3_NM_006922 | (101) | RFSATSALYILTPINPVRKIAKILVHSLFSMLIMCTILTNCVFMTLSP |
| hNav1.3_AF225986 | (101) | RFSATSALYILTPINPVRKIAKILVHSLFSMLIMCTILTNCVFMTLSP |
| rNav1.3_NM_013119 | (101) | RFSATSALYILTPINPVRKIAKILVHSLFSMLIMCTILTNCVFMTLSP |
| mNav1.3 wild-type | (151) | PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLD FSVIVM |
| hNav1.3_NM_006922 | (151) | PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLD FSVIVM |
| hNav1.3_AF225986 | (151) | PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLD FSVIVM |
| rNav1.3_NM_013119 | (151) | PDWTKNVEYTFGIYTFESLIKILARGFCLEDFTELDPNNWLD FSVIVM |
| mNav1.3 wild-type | (201) | AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTI VGALIQSVKKLSDV |
| hNav1.3_NM_006922 | (201) | AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTI VGALIQSVKKLSDV |
| hNav1.3_AF225986 | (201) | AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTI VGALIQSVKKLSDV |
| rNav1.3_NM_013119 | (201) | AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTI VGALIQSVKKLSDV |
| mNav1.3 wild-type | (251) | MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD |
| hNav1.3_NM_006922 | (251) | MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD |
| hNav1.3_AF225986 | (251) | MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD |
| rNav1.3_NM_013119 | (251) | MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD |

FIG. 1

| | | |
|-------------------|-------|--------------------------------------------------------|
| mNav1.3 wild-type | (301) | SNGTFVNVITMSTFNWKDYI |
| hNav1.3_NM_006922 | (301) | SNGTFVNVITMSTFNWKDYI |
| hNav1.3_AF225986 | (301) | SNGTFVNVITMSTFNWKDYI |
| rNav1.3_NM_013119 | (301) | SNGTFVNVITMSTFNWKDYI |
| mNav1.3 wild-type | (351) | ICVKAGRNPNGYTSFDTSWAFSLFRLMTQDYWENLYQLTLRAAGKTY |
| hNav1.3_NM_006922 | (351) | ICVKAGRNPNGYTSFDTSWAFSLFRLMTQDYWENLYQLTLRAAGKTY |
| hNav1.3_AF225986 | (351) | ICVKAGRNPNGYTSFDTSWAFSLFRLMTQDYWENLYQLTLRAAGKTY |
| rNav1.3_NM_013119 | (351) | ICVKAGRNPNGYTSFDTSWAFSLFRLMTQDYWENLYQLTLRAAGKTY |
| mNav1.3 wild-type | (401) | MIFFVLVIFLGSEFVILVNLILAVVAMAYEEQNOATILEEAEQKEAEFQOQMLE |
| hNav1.3_NM_006922 | (401) | MIFFVLVIFLGSEFVILVNLILAVVAMAYEEQNOATILEEAEQKEAEFQOQMLE |
| hNav1.3_AF225986 | (401) | MIFFVLVIFLGSEFVILVNLILAVVAMAYEEQNOATILEEAEQKEAEFQOQMLE |
| rNav1.3_NM_013119 | (401) | MIFFVLVIFLGSEFVILVNLILAVVAMAYEEQNOATILEEAEQKEAEFQOQMLE |
| mNav1.3 wild-type | (451) | QLKKQEEAQAVAAASASRDFTSC |
| hNav1.3_NM_006922 | (451) | QLKKQEEAQAVAAASASRDFTSC |
| hNav1.3_AF225986 | (451) | QLKKQEEAQAVAAASASRDFTSC |
| rNav1.3_NM_013119 | (451) | QLKKQEEAQAVAAASASRDFTSC |
| mNav1.3 wild-type | (501) | NRRKKRRQREHLEGNH |
| hNav1.3_NM_006922 | (501) | NRRKKRRQREHLEGNH |
| hNav1.3_AF225986 | (501) | NRRKKRRQREHLEGNH |
| rNav1.3_NM_013119 | (501) | NRRKKRRQREHLEGNH |
| mNav1.3 wild-type | (551) | KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST |
| hNav1.3_NM_006922 | (551) | KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST |
| hNav1.3_AF225986 | (551) | KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST |
| rNav1.3_NM_013119 | (551) | KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGAKDVGSENDFADEHST |

FIG. 1

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|-------------------|-------|------------------------|------------------------------------|
| mNav1.3 wild-type | (601) | FEDSESRRDLSLFVPHR | GERRNSNVSOASMSRRMVPGLPANGKMHSTVDC |
| hNav1.3_NM_006922 | (601) | FEDGESRRDLSLFVPHR | HGERRNSNVSOASMSRRMVPGLPANGKMHSTVDC |
| hNav1.3_AF225986 | (601) | FEDSESRRDLSLFVPHR | HGERRNSN----- |
| rNav1.3_NM_013119 | (601) | FEDSESRRDLSLFVPHR | GERRNSN----- |
| mNav1.3 wild-type | (651) | NGVVSIL----- | GTTTETEVKRRLLSSYOISMEMLEDSS |
| hNav1.3_NM_006922 | (651) | NGVVSILVGGPSALTSPTGQLP | PEGTTTETEVKRRLLSSYOISMEMLEDSS |
| hNav1.3_AF225986 | (625) | ----- | GTTTETEVKRRLLSSYOISMEMLEDSS |
| rNav1.3_NM_013119 | (625) | ----- | GTTTETEVKRRLLSSYOISMEMLEDSS |
| mNav1.3 wild-type | (684) | GRQRANSIASILNTNMEEL | LEESRQKCPPCWYRFANVFLIWDCCD |
| hNav1.3_NM_006922 | (701) | GRQRANSIASILNTNMEEL | LEESRQKCPPCWYRFANVFLIWDCCD |
| hNav1.3_AF225986 | (652) | GRQRANSIASILNTNMEEL | LEESRQKCPPCWYRFANVFLIWDCCD |
| rNav1.3_NM_013119 | (652) | GRQRANSIASILNTNMEEL | LEESRQKCPPCWYRFANVFLIWDCCD |
| mNav1.3 wild-type | (734) | HLVNLIVMDPFVDLAI | TICIVLNTLFMAMEHYPMTEQFSSVLT |
| hNav1.3_NM_006922 | (751) | HLVNLIVMDPFVDLAI | TICIVLNTLFMAMEHYPMTEQFSSVLT |
| hNav1.3_AF225986 | (702) | HLVNLIVMDPFVDLAI | TICIVLNTLFMAMEHYPMTEQFSSVLT |
| rNav1.3_NM_013119 | (702) | HLVNLIVMDPFVDLAI | TICIVLNTLFMAMEHYPMTEQFSSVLT |
| mNav1.3 wild-type | (784) | GIFTAEMVLKIIANDP | YYYFQEGWNIFDGIIVSLSLMELGLNVEGLSVL |
| hNav1.3_NM_006922 | (801) | GIFTAEMVLKIIANDP | YYYFQEGWNIFDGIIVSLSLMELGLNVEGLSVL |
| hNav1.3_AF225986 | (752) | GIFTAEMVLKIIANDP | YYYFQEGWNIFDGIIVSLSLMELGLNVEGLSVL |
| rNav1.3_NM_013119 | (752) | GIFTAEMVLKIIANDP | YYYFQEGWNIFDGIIVSLSLMELGLNVEGLSVL |
| mNav1.3 wild-type | (834) | RSFRLIRVFKLAKSWPT | INMLIKIIGNSVGALGNLTIVLAIIVFIFAVVG |
| hNav1.3_NM_006922 | (851) | RSFRLIRVFKLAKSWPT | INMLIKIIGNSVGALGNLTIVLAIIVFIFAVVG |
| hNav1.3_AF225986 | (802) | RSFRLIRVFKLAKSWPT | INMLIKIIGNSVGALGNLTIVLAIIVFIFAVVG |
| rNav1.3_NM_013119 | (802) | RSFRLIRVFKLAKSWPT | INMLIKIIGNSVGALGNLTIVLAIIVFIFAVVG |
| mNav1.3 wild-type | (884) | MQLFGKSYKEVCVKIN | DCKLPRWHMDFHFSFLIVFRLCGEWIETMWD |

FIG. 1

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|-------------------|--------|----------------------|-------------------------|-------------------------------|
| hNav1.3_NM_006922 | (901) | MQLFGKSYKEVCVKINDDC | LPWHMNDFFHSFLIVFRVLCGEW | IETMWD |
| hNav1.3_AF225986 | (852) | MQLFGKSYKEVCVKINDDC | LPWHMNDFFHSFLIVFRVLCGEW | IETMWD |
| rNav1.3_NM_013119 | (852) | MQLFGKSYKEVCVKINVDCK | LPWHMNDFFHSFLIVFRVLCGEW | IETMWD |
| mNav1.3_wild-type | (934) | CMEVAGQTMCLIVFMLVMV | IGNLVVNLFLALLSSFS | SSDNLAAATDDDNE |
| hNav1.3_NM_006922 | (951) | CMEVAGQTMCLIVFMLVMV | IGNLVVNLFLALLSSFS | SSDNLAAATDDDNE |
| hNav1.3_AF225986 | (902) | CMEVAGQTMCLIVFMLVMV | IGNLVVNLFLALLSSFS | SSDNLAAATDDDNE |
| rNav1.3_NM_013119 | (902) | CMEVAGQTMCLIVFMLVMV | IGNLVVNLFLALLSSFS | SSDNLAAATDDDNE |
| mNav1.3_wild-type | (984) | MNNLQIAVGRMOKGIDV | VKNLRECFKAFRKPKV | IEIHEGNKIDSCMS |
| hNav1.3_NM_006922 | (1001) | MNNLQIAVGRMOKGIDV | VKNLRECFKAFRKPKV | IEIHEGNKIDSCMS |
| hNav1.3_AF225986 | (952) | MNNLQIAVGRMOKGIDV | VKNLRECFKAFRKPKV | IEIHEGNKIDSCMS |
| rNav1.3_NM_013119 | (952) | MNNLQIAVGRMOKGIDV | VKNLRECFKAFRKPKV | IEIHEGNKIDSCMS |
| mNav1.3_wild-type | (1034) | NNTG | EISKELNYLDGNGTTS | GVGTGSSVEKYVIDENDYMSFINNPSL |
| hNav1.3_NM_006922 | (1051) | NNTG | EISKELNYLDGNGTTS | GVGTGSSVEKYVIDENDYMSFINNPSL |
| hNav1.3_AF225986 | (1002) | NNTG | EISKELNYLDGNGTTS | GVGTGSSVEKYVIDENDYMSFINNPSL |
| rNav1.3_NM_013119 | (1002) | NNTG | EISKELNYLDGNGTTS | GVGTGSSVEKYVIDENDYMSFINNPSL |
| mNav1.3_wild-type | (1084) | TVTVP | IAVGESDPENLNT | EEFSSELEESKEKINATSSSEGSTVDVLP |
| hNav1.3_NM_006922 | (1100) | TVTVP | IAVGESDPENLNT | EEFSSELEESKEKINATSSSEGSTVDVLP |
| hNav1.3_AF225986 | (1051) | TVTVP | IAVGESDPENLNT | EEFSSELEESKEKINATSSSEGSTVDVLP |
| rNav1.3_NM_013119 | (1051) | TVTVP | IAVGESDPENLNT | EEFSSELEESKEKINATSSSEGSTVDVLP |
| mNav1.3_wild-type | (1134) | REGQAE | IEPEEDKPEACFTGECIKKFP | FCQVSTEEGKGIWNNLRKTC |
| hNav1.3_NM_006922 | (1150) | REGQAE | IEPEEDKPEACFTGECIKKFP | FCQVSTEEGKGIWNNLRKTC |
| hNav1.3_AF225986 | (1101) | REGQAE | IEPEEDKPEACFTGECIKKFP | FCQVSTEEGKGIWNNLRKTC |
| rNav1.3_NM_013119 | (1101) | REGQAE | IEPEEDKPEACFTGECIKKFP | FCQVSTEEGKGIWNNLRKTC |
| mNav1.3_wild-type | (1184) | YSIVEHNWFET | PIVFMILLSSGALAFEDI | YIEQRKTIKIMLEYADKVFTY |
| hNav1.3_NM_006922 | (1200) | YSIVEHNWFET | PIVFMILLSSGALAFEDI | YIEQRKTIKIMLEYADKVFTY |

FIG. 1

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|-------------------|--------|------------------------------------------------------|
| hNav1.3_AF225986 | (1151) | YSIVEHNNFFETFIIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY |
| rNav1.3_NM_013119 | (1151) | YSIVEHNNFFETFIIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY |
| mNav1.3 wild-type | (1234) | IFILEMILKWAAYGFQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA |
| hNav1.3_NM_006922 | (1250) | IFILEMILKWAAYGFQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA |
| hNav1.3_AF225986 | (1201) | IFILEMILKWAAYGFQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA |
| rNav1.3_NM_013119 | (1201) | IFILEMILKWAAYGFQTYFTINAWCWLDFLIYDVSLVSLVANALGYSELGA |
| mNav1.3 wild-type | (1284) | IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPIIMNVLLVCLIFWLIF |
| hNav1.3_NM_006922 | (1300) | IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPIIMNVLLVCLIFWLIF |
| hNav1.3_AF225986 | (1251) | IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPIIMNVLLVCLIFWLIF |
| rNav1.3_NM_013119 | (1251) | IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPIIMNVLLVCLIFWLIF |
| mNav1.3 wild-type | (1334) | SIMGVNLFAGKFYHCVNMTTGGNMFDSVNNFSDCOALGKQARWKNVKVN |
| hNav1.3_NM_006922 | (1350) | SIMGVNLFAGKFYHCVNMTTGGNMFDSVNNFSDCOALGKQARWKNVKVN |
| hNav1.3_AF225986 | (1301) | SIMGVNLFAGKFYHCVNMTTGGNMFDSVNNFSDCOALGKQARWKNVKVN |
| rNav1.3_NM_013119 | (1301) | SIMGVNLFAGKFYHCVNMTTGGNMFDSVNNFSDCOALGKQARWKNVKVN |
| mNav1.3 wild-type | (1384) | FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV |
| hNav1.3_NM_006922 | (1400) | FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV |
| hNav1.3_AF225986 | (1351) | FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV |
| rNav1.3_NM_013119 | (1351) | FDNVGAGYLALLQVATFKGWMIMYAAVDSRDVKLQPVYEENLYMYLYFV |
| mNav1.3 wild-type | (1434) | IFIIFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYYNAMKKL |
| hNav1.3_NM_006922 | (1450) | IFIIFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYYNAMKKL |
| hNav1.3_AF225986 | (1401) | IFIIFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYYNAMKKL |
| rNav1.3_NM_013119 | (1401) | IFIIFGSFFTLNFIIGVIIDNFNOOKKKFGGQDIFWTEEQKKYYNAMKKL |
| mNav1.3 wild-type | (1484) | GSKKPQKPIPRPANKFQGMVDFVTRQVDFISIMILICLNMTMMVETDD |
| hNav1.3_NM_006922 | (1500) | GSKKPQKPIPRPANKFQGMVDFVTRQVDFISIMILICLNMTMMVETDD |
| hNav1.3_AF225986 | (1451) | GSKKPQKPIPRPANKFQGMVDFVTRQVDFISIMILICLNMTMMVETDD |

FIG. 1

| | | |
|-------------------|--------|------------------------------------------------------------------------------------------------------------------------------|
| rNav1.3_NM_013119 | (1451) | GSKPKPKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVMMVETDD |
| mNav1.3 wild-type | (1534) | QKYM TL VL SR INL VF IVLFTGEF ILKL SLR YY FTTIGNIFDFV VVIL |
| hNav1.3_NM_006922 | (1550) | QKYM TL VL SR INL VF IVLFTGEF ILKL SLR YY FTTIGNIFDFV VVIL |
| hNav1.3_AF225986 | (1501) | QKYM TL VL SR INL VF IVLFTGEF ILKL SLR YY FTTIGNIFDFV VVIL |
| rNav1.3_NM_013119 | (1501) | QKYM TL VL SR INL VF IVLFTGEF ILKL SLR YY FTTIGNIFDFV VVIL |
| mNav1.3 wild-type | (1584) | SIVGMFLAELIEKYFVSPTLFRVIRLARIGRI RL IKGAKGIR TLL FALM |
| hNav1.3_NM_006922 | (1600) | SIVGMFLAELIEKYFVSPTLFRVIRLARIGRI RL IKGAKGIR TLL FALM |
| hNav1.3_AF225986 | (1551) | SIVGMFLAELIEKYFVSPTLFRVIRLARIGRI RL IKGAKGIR TLL FALM |
| rNav1.3_NM_013119 | (1551) | SIVGMFLAELIEKYFVSPTLFRVIRLARIGRI RL IKGAKGIR TLL FALM |
| mNav1.3 wild-type | (1634) | MSLPALFNIGLILLFLVMFIYALFGMSNFAYVKKKEAGIDDMFNFTFGNSM |
| hNav1.3_NM_006922 | (1650) | MSLPALFNIGLILLFLVMFIYALFGMSNFAYVKKKEAGIDDMFNFTFGNSM |
| hNav1.3_AF225986 | (1601) | MSLPALFNIGLILLFLVMFIYALFGMSNFAYVKKKEAGIDDMFNFTFGNSM |
| rNav1.3_NM_013119 | (1601) | MSLPALFNIGLILLFLVMFIYALFGMSNFAYVKKKEAGIDDMFNFTFGNSM |
| mNav1.3 wild-type | (1684) | ICLFQITTSAGWDGHLAPILNSAPPCDPPDAIHPGSSVKGDCG PSVGIF |
| hNav1.3_NM_006922 | (1700) | ICLFQITTSAGWDGHLAPILNSAPPCDPPDAIHPGSSVKGDCG PSVGIF |
| hNav1.3_AF225986 | (1651) | ICLFQITTSAGWDGHLAPILNSAPPCDPPDAIHPGSSVKGDCG PSVGIF |
| rNav1.3_NM_013119 | (1651) | ICLFQITTSAGWDGHLAPILNSAPPCDPPDAIHPGSSVKGDCG PSVGIF |
| mNav1.3 wild-type | (1734) | FFVS YII ISFLV VNM YIAVILENFSVATERSAEPLSEDDFEMFYEVWEK |
| hNav1.3_NM_006922 | (1750) | FFVS YII ISFLV VNM YIAVILENFSVATERSAEPLSEDDFEMFYEVWEK |
| hNav1.3_AF225986 | (1701) | FFVS YII ISFLV VNM YIAVILENFSVATERSAEPLSEDDFEMFYEVWEK |
| rNav1.3_NM_013119 | (1701) | FFVS YII ISFLV VNM YIAVILENFSVATERSAEPLSEDDFEMFYEVWEK |
| mNav1.3 wild-type | (1784) | FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDR IHC |
| hNav1.3_NM_006922 | (1800) | FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDR IHC |
| hNav1.3_AF225986 | (1751) | FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDR IHC |
| rNav1.3_NM_013119 | (1751) | FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDR IHC |

FIG. 1

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|-------------------|--------|------------------|-----------------------|--------------------|
| mNav1.3 wild-type | (1834) | LDILFAFTKRVL | ESGEMDALRIQMEDRFMASNP | SKVSYEPITTTTLKRKQ |
| hNav1.3_NM_006922 | (1850) | LDILFAFTKRVL | ESGEMDALRIQMEDRFMASNP | SKVSYEPITTTTLKRKQ |
| hNav1.3_AF225986 | (1801) | LDILFAFTKRVL | ESGEMDALRIQMEDRFMASNP | SKVSYEPITTTTLKRKQ |
| rNav1.3_NM_013119 | (1801) | LDILFAFTKRVL | ESGEMDALRIQMEDRFMASNP | SKVSYEPITTTTLKRKQ |
| mNav1.3 wild-type | (1884) | EEVSAAI IQRN | RCYLLKQRLKNISNTYDKH | IKGRIVLPKGDMA IDKL |
| hNav1.3_NM_006922 | (1900) | EEVSAAI IQRN | RCYLLKQRLKNISNTYDKH | IKGRIVLPKGDMA IDKL |
| hNav1.3_AF225986 | (1851) | EEVSAAI IQRN | RCYLLKQRLKNISNTYDKH | IKGRIVLPKGDMA IDKL |
| rNav1.3_NM_013119 | (1851) | EEVSAAI IQRN | RCYLLKQRLKNISNTYDKH | IKGRIVLPKGDMA IDKL |
| mNav1.3 wild-type | (1934) | NGNSTPEKTDGSSSTT | PPPSYDSVTKPDKEKFEKD | KPEKSKGKEV --- |
| hNav1.3_NM_006922 | (1950) | NGNSTPEKTDGSSSTT | PPPSYDSVTKPDKEKFEKD | KPEKSKGKEVRENQ |
| hNav1.3_AF225986 | (1901) | NGNSTPEKTDGSSSTT | PPPSYDSVTKPDKEKFEKD | KPEKSKGKEVRENQ |
| rNav1.3_NM_013119 | (1901) | NGNSTPEKTDGSSSTT | PPPSYDSVTKPDKEKFEKD | KPEKSKGKEVRENQ |
| mNav1.3 wild-type | (1980) | -- | | |
| hNav1.3_NM_006922 | (2000) | K- | | |
| hNav1.3_AF225986 | (1951) | K- | | |
| rNav1.3_NM_013119 | (1951) | K- | | |

FIG. 2

ALIGNMENT OF FULL-LENGTH AND PARTIAL MOUSE Nav1.3 PROTEIN

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|-------------------|-------|-------------------------------------------|
| mNav1.3 wild-type | (1) | MAQALLVPPGPSPSFRLLFTRESIAAIEKRAAEKAKKPKKE |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (41) | QDIDDENKPKNSDLEAGKNLPFIYGDIPPEMVSEPLEDL |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (81) | DPYVSKKTFVVLNKGKAIFFRSATSALYILTPLNPVKKI |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (121) | AIKILVHSLFSLIMCTILTNCVFMTLSPDPDWTKNVEYT |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (161) | FTGIYTFESLIKILARGECLFEDFTFLRDPWNWLDFSVIVM |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (201) | AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIIVGAL |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (241) | IQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLOW |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (281) | PPSDSAFEINTSYFNGMTDSNGTFFNVVTMSTFNWKDYIA |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (321) | DDSHFYVLDGQKDPILLCGNGSDAGQCPEGYICVKAGRPN |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (361) | YGYSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY |
| mNav1.3 NM_018732 | | ----- |

FIG. 2

| | |
|----------------------------------------|-----------------------------------------------------------|
| mNav1.3 wild-type mNav1.3 NM_018732 | (401) MIEFFVLVIFLGSFYLVNLLILAVVAMAYEEQNQATLEEAEQ ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (441) KEAEFQQMLEQLKKQEEAQAVAAASAASRDFSGIGGLGE ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (481) LLESSEASKLSSKSAKEWNRKRKRRQREHLEGNHRPEG ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (521) DRFPKSESEDSVKRRSFLFSLDGNPLSGDKKLCSPHQSIIL ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (561) SIRGSLFSPRNSKTSIFSFRGRAKDVGSENFADDEHST ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (601) FEDSESRDLSLFVPHRPGERRNSNVQASMSRMPGLPA ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (641) NGKMHSTVDCNGVVSGLGTTTETEVKRRRLSSYQISMEMLE ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (681) DSSGRQAMSTASILTNTMEELEESRQKCPPCWYRFANVF ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (721) LIWDCCDSWLKVKHLVNLIIVMDPFVDLAIICIVLNTLFM ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (761) AMEHYPMTEQFSSVLTVGNLVFTGIFTAEWVLKIIAMDPY ----- |
| mNav1.3 wild-type mNav1.3 NM_018732 | (801) YYFQEGWNIFDGIIVSLSLMELGLANVEGLSVLRSFRLIR ----- |

FIG. 2

| | | |
|-------------------|--------|--------------------------------------------|
| mNav1.3 wild-type | (841) | VFKIAKSWPTLNMLIKIIGNSVGALGNLTILVLAIIIVFIFA |
| mNav1.3 NM_018732 | (1) | -----MLIKIIGNSVGALGNLTILVLAIIIVFIFA |
| mNav1.3 wild-type | (881) | VVGQQLFGKSYKEVCCKINEDCKLPRWHMNDFFHSFLIVF |
| mNav1.3 NM_018732 | (29) | VVGQQLFGKSYKEVCCKINEDCKLPRWHMNDFFHSFLIVF |
| mNav1.3 wild-type | (921) | RVLGGEWIEIWMDCMEVAGQTMCLIVFMLVMVIGNLVVLN |
| mNav1.3 NM_018732 | (69) | RVLGGEWIEIWMDCMEVAGQTMCLIVFMLVMVIGNLVVLN |
| mNav1.3 wild-type | (961) | LFLALLSSFSDDNLAATDDDDNEMNNLQIAYGRMOKGIDY |
| mNav1.3 NM_018732 | (109) | LFLALLSSFSDDNLAATDDDDNEMNNLQIAYGRMOKGIDY |
| mNav1.3 wild-type | (1001) | VKNKIRECFRKAFRRKPKVIEIHEGNKIDSCMSNNTGVVE |
| mNav1.3 NM_018732 | (149) | VKNKIRECFRKAFRRKPKVIEIHEGNKIDSCMSNNTGVVE |
| mNav1.3 wild-type | (1041) | ISKELNYLKDNGTTSVGVTGSSVEKVIIDENDYMSFINN |
| mNav1.3 NM_018732 | (189) | ISKELNYLKDNGTTSVGVTGSSVEKVIIDENDYMSFINN |
| mNav1.3 wild-type | (1081) | PSLTIVTVPIAVGESDFENLNTFEFSSESELESKEKLNAT |
| mNav1.3 NM_018732 | (229) | PSLTIVTVPIAVGESDFENLNTFEFSSESELESKEVSALF |
| mNav1.3 wild-type | (1121) | SSSEGSTVDVAPPREGEQAEPEEDLKPEACFTEGCIKK |
| mNav1.3 NM_018732 | (269) | SSGHHFCAIYTVWLLCIVFC----- |
| mNav1.3 wild-type | (1161) | FPFCQVSTEEGKGKIWNLRKTCYSIVEHNNWETFIVFMI |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1201) | ILSSGALAFEDIYIEHQRTIKTMLEYADKVFTYIFILEML |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1241) | LKWVAYGFQTYFTNACWLDFLIVDVSLVSLVANALGYSE |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1281) | LGAIKSLRTILRALRPLRALSRFEGMRVVVNALVGAIPSIM |

FIG. 2

| | |
|-------------------|--------------------------------------------------|
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1321) NVLLVCLIFWLIFSIMGVNLFAGKFYHCVMNMTTGSMTDMS |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1361) EVNNSDCQALGKQARWKNVKNFDNVGAGYLALLQVATF |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1401) KGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVFIIFGS |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1441) FFTLNLFIGVIIDNFNQKKKFGGQDIFMTEEQKKYYNAM |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1481) KKLGSKKPKPIPRPANKFOGMVDFVTRQVFDISIMILI |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1521) CLNMVTMMVETDDQSKYMTLVLSRINLVFIVLFTGEFLIK |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1561) LISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1601) PTLFRVIRLARIGRIILRLIKGAKGIRTLFLAIMMSLPALF |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1641) NIGLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFTFPG |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1681) NSMICLFQITTSAGWDGILLAPIINSAPPDPCDPAIHGSS |
| mNav1.3 NM_018732 | ----- |
| mNav1.3 wild-type | (1721) VKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSV |
| mNav1.3 NM_018732 | ----- |

FIG. 2

| | | |
|-------------------|--------|-------------------------------------------|
| mNav1.3 wild-type | (1761) | ATERSAEPLSEDDFEMFYEVWEKFPDPAQTFIEFCKLSDF |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1801) | AAALDPPLLIAPKNKVQLIAMDLPMVSGDRIHCLDILFAF |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1841) | TKRVIGESGEMDAIRIQMEDREFMASNPskVSEPIITTLK |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1881) | RQEEVSAAIIQRNYRCYLLKQRLKNISNTYDKETIKGRI |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1921) | VLPIKGDWVIDKLNNGNSTPEKTDGSSSTTSPPSYDSVTKP |
| mNav1.3 NM_018732 | | ----- |
| mNav1.3 wild-type | (1961) | DKEKFEKDKPEKESKGKEV |
| mNav1.3 NM_018732 | | ----- |

FIG. 3

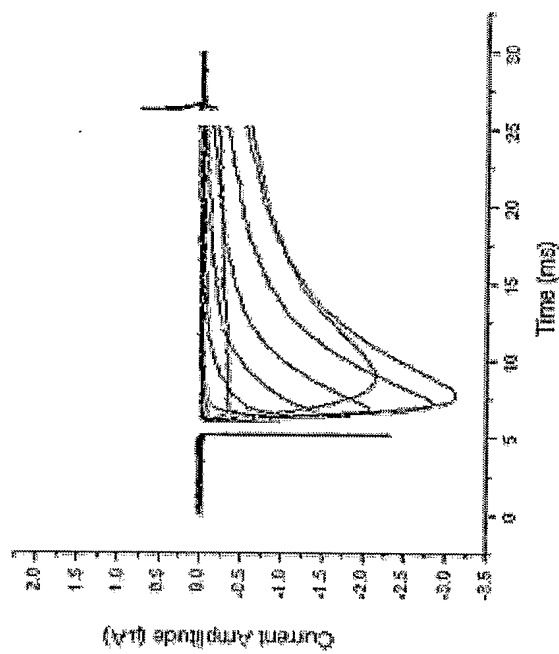


FIG. 4

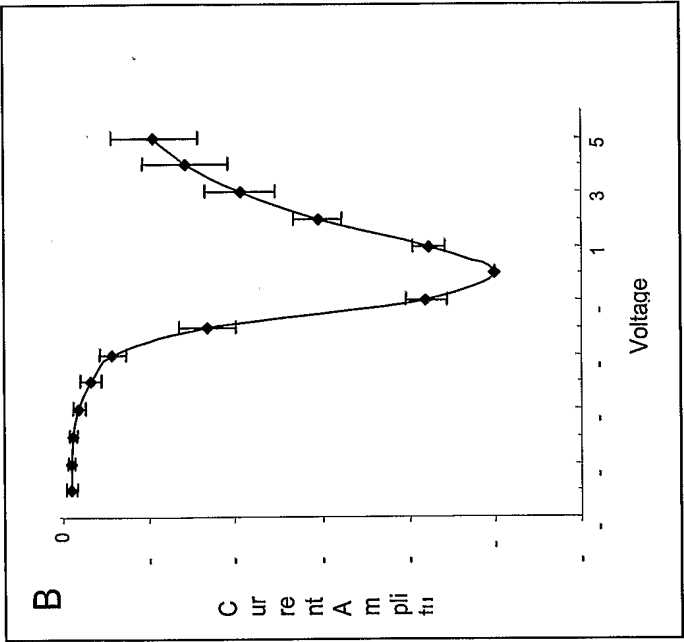


FIG. 5

SEQ ID NO:1

ATGGCCAGGCACTGCTGGTACCCCGGGACCTGAGAGCTTCC
 GCCTTTTCACTCGAGAATCTCTTGCTGCTATCGAAAAAGCGTGTGTCAGAA
 GAGAAAGCCAAAGAAACCCAAAGAAAGAACAGACATTGACGATGAGAACAA
 GCCAAAGCCAAACAGTGACTTGGAGCTGGAGAACCTTCCATTATCT
 ATGGAGACATTCCTCCAGAGATGGTGTGAGAGCCTCTGGAGGACCTGGAC
 CCTACTACGTCAGTAAGAAAACCTTTGTAGTGTGAATAAAGGGGAGGC
 AATTTTCGATTCAGTGCACCTCCGCTGTGTATATTTAACTCCACTAA
 ACCCGTTAGGAAAATTGCTATTAAAGATTTGGTACACTCTTTATTTCAGC
 ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTATGACATTGAG
 CAATCCTCCTGACTGGACGAAGAAATGTAGAGTACACATTCACTGGGATCT
 ATACCTTTGAGTCACCTATAAAGATCTTGGCCAGAGGATTCGTTAGAA
 GATTTCACTTCTTCTGTGACCCATGGAACTGGCTGGATTCAGTGTCAAT
 CTGATGGCATATGTGACAGAGTTTGTGACCTGGGCAATGTCTCAGCGC
 TGAGAAAGTTTCAGAGTTCTCGAGCATTAAGAAACAAATACAGTCAATCCA
 GGTTTAAAGACCATCGTGGGGCCCTGATCCAGTCGGTGAAGAGCTGTC
 TGACGTCAATGATACTCACTGTGTCTGTCTGAGCGTCTTTGCTCTCATCG
 GGTGTCAGCTCTTCATGGCAACCTGAGGAATAAATGCTTGCAGTGGCT
 CCAAGCGATTCGCTTTTGAGATCAACACTACTTCTTCAATGGCAC
 AATGGAATCAATGGGACATTTGTAAATGTAAACAATGAGCACATTCAACT
 GGAAGGACTATATCGCAGATGACAGCCACTTTTATGTTTGGATGGACAA
 AAAGATCCTTTACTTTGTGAAATGGGTCCGATGCAGACAAATGTCCAGA
 AGGGTACATCTGTGTGAAGCTGGACGAACCCCACTACGGTTACAGA
 GCTTTGACACATTTAGCTGGGCCCTTCTTATCGCTGTTTCGACTCATGACT
 CAAGACTACTGGGAGAACCTTACCAGTTGACATTAAGTGCAGCTGGGAA
 AACCTACATGATCTTTTCTGCTGTTAAATTTCTTGGGCTCATTTTATT
 TGGTGAACTTGTATCCTGGCTGTGGTGGCCATGGCCATGAGGAAACAAAT
 CAGGCCACACTGGAGGAGCTGAGCAGAAAGAGCGGAGTTTTCAGCAGAT
 GTTGGAGCAGTTGAAAGAGCAGAGAGGCTCAGGCGGTGGCAGCTG
 CCTCAGCAGCGCTCCAGAGACTTCAGTGGGATAGGAGGTTAGGAGAACTT
 CTGGAGAGTTCTTCAGAAAGCTTCCAAGTTGAGCTCCAAGAGTGCAGGA
 GTGGAGGAATCGGAGGAAGAAAGAGGAGACAGAGGGGACCTTGGAGGGAA

FIG. 5

ACCACAGACCCGAAGGAGACAGGTTTCCCAAGTCGGAAATCAGAAGACAGC
GTCAAGCGAAGGAGTTTCTGTGTTCTCCCTGGATGGGAACCCGCTGAGCGG
CGACAAGAAGCTGTGCTCTCCCATCAGTCTCTCTTGAGTATCCGTGGCT
CCCTGTTTCCCAAGACGCAATAGCAAAACGAGCATTTTCAGCTTCAGA
GGTCGGCGGAAGGACGTGGGTCTGAGAAATGACTTTGCGGATGATGAACA
CAGACACTTTTGAAGATAGCAGAGACGAGAGAGACTCACTGTTTGTGCGGC
ACAGACCTGGAGAGCGACGCAACAGTAACGTTAGTCAGGCCAGTATGTCA
TCCAGGATGGTGCCAGGGCTTCCAGCCAAATGGGAAGATGCACAGCACTGT
GGATTGCAATGGTGTGTTTCTTGGGTACCACTGTAAGAAATGCTGGAGGAT
GGAAGAGAAGGCTAAGTTCTTACCAGATCTCGATGGAATGCTGGAGGAT
TCCTCTGGGAGACAAAGACCATGAGCATAGCCAGTATCCTGACCAACAC
GATGGAGGAACCTTGAAGAACTTAGACAGAAGTGTCCACCATGCTGTGTATA
GATTTGCCAATGTGTTTGTGATCTGGGACTGTTGTGATTCATGGTTGAAA
GTAAAGCATCTTGTGAATTTGATTTGATTTGATGGATCCATTTGTTGACCTGGC
CATCACCATCTGTCATCGTGTAAACACACTGTTTCATGGCCATGGAGCACT
ACCCGATGACGGAGCAGTTCAGCAGTGTGCTGACGGTGGGAAACCTGGTC
TTCACGGGATCTTCAAGCCGAGATGGTCTTGAATAATCATCGCAATGGA
TCCCTATTACTATTTCGAAGAGGCTGGAATATCTTTGATGGAATATTG
TTAGCCTGAGTTTAAATGAGCTTGGCCCTGGCAACCGTGGAGGGGCTGTCC
GTGCTTCGCTCCTTCAGACTGTGCGAGTCTTCAAGTTGGCAAAATCCTG
GCCACACTGAATATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCAC
TGGGCAACCTGACCTGCTGCTGGCCATCATCGTCTTCATTTTGGCGTG
GTCGGCATGAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTTTGCAAGAT
CAATGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACT
CCTTCTGATAGTGTTCGCGTGTGTTGGGCGCAGACCATGTGCTTATTTGTGTTAT
TGGGACTGCGATGGAGTCCGCGGCGCAGACCATGTGCTTATTTGTGTTAT
GTTGTCATGGTGATTGGGAACCTTGTGTTCTGAACCTCTTCTGCGCT
TATTGTTGAGTCTTTAGTTTCAACAACCTTGTGCTACGGACGATGAT
AACGAAATGAACAACCTCCAGATCGCGTGGGAAGGATGCAAAAGGGGAT
TGATTATGTGAAAATAAAGATACGGGAGTGTCTCCGAAAAGCGTTTTTTA
GAAAGCCGAAAGTATAGAAATCCACGAAGGGAACAAAATAGACAGCTGC
ATGTCCAATAACACGGGCGTAGTTGAAATAAGCAAGAGCTTAACCTACCT
TAAAGACGGTAACGGAAACCAACCACTGGGTGGGTACTGGAAGCAGTGTGG

FIG. 5

AGAAATACGTAATTGATGAAAATGACTACATGTCTATTCTCATCAACAACCCC
 AGCTCACCGTGACGGTGCCTAATGCGTGGGAGAGTCTGACTTTTGAAAA
 TTTTAAACACGGAAGAGTTTAGCAGTGAATCAGAACTGGAAAGAAAGCAAGG
 AGAAATTAAATGCAACCAAGCTCTTTCTGAAGAAAGCACAGTTGACGTTGCT
 CCGCCCCGAGAGGTGAACAAGCTGAAATGAACCTGAGGAGGACCTTAA
 GCCAGAAGCTTGTCTTACTGAAGGATGCATTAAAAATTTCCCTTCTGCC
 AAGTAAGTACGGAAGAAGTAAAGGAAAAATCTGGTGAATCTTAGGAAG
 ACCTGCTATAGCATGTGGAACACAACCTGGTTTGAGACCTTCATTGTCTT
 CATGATTCTCCTCAGTAGTGGTGCTTTGGCTTTGAAGATATATACATTG
 AGCAACGGAAGAACCATCAAAACCATGCTGGAGTATGCTGACAAAAGCTTTC
 ACTTACATCTTTCATCTCTGGAAATGCTCCTCAAAATGGGTGGCCTATGGATT
 TCAAAACCTATTTCAACCAATGCCCTGGTCTGGTTGGACCTTCTTGAATTGTTG
 ATGTTCTTTTGGTTAGCTTGGTGGCCACGCTCTTTGGCTATTTCAGAACTT
 GGTGCCATCAAAATCCCTACGACCCCTGAGAGCTCTGAGGCCGCTCCGAGC
 CTTATCCCGCTTGAAGGCATGAGGGTGGTTGTGAACGCTCTTGTGGTG
 CAATCCCCTCCATCATGAATGTGCTACTGGTGTGCCCTCATCTTCTGGTTA
 ATCTTTAGTATCATGGGTGTAATCTGTTTGTCTGGAAGTTCTATCACTG
 TGTAAACATGACAACGGGCAGCATGTTTCGACATGAGTGAAGTCAACAATT
 TCAGCGACTGTGAGGCTCTTGGCAAGCAAGCCCGATGGAAGAATGTGAAA
 GTCAACTTTGACAAATGTTGGGCTGGCTACCTGGCATTGTGCAAGTGGC
 CACATTCAAAGGCTGGATGGATATTATGTATGCAGCTGTGGATTACGGG
 ACGTCAAACTGCAGCCTGTATATGAAGAAATCTGTAACATGTATCTGTAC
 TTTGTCTATCTTTCATCATCTTTGGTCTGTTCTTCACTCTAAATCTATTCTAT
 CGGCGTCACTATAGACAACCTTCAACCCAGCAGAAAGAAAGTTTGGAGGTC
 AAGACATCTTTATGACAGAAGAGCAGAAAAAGTACTACAATGCAATGAAG
 AAACCTTGGCTCCAAAAAACCCTCAGAAGCCATCCCTCGACCTGCACAA
 ATTTCAAGGAATGGTCTTTGACTTTTGAACCAAGCAAGTGTGACATCA
 GCATCATGATCTCTCATCTGCCCTCAACATGGTGACCATGATGGTGGAAACG
 GAGACCCAGAGCAAAATACATGACCCCTGGTTTTGTCCCGAATCAACCTGGT
 ATTCATCGTCTCTTCTACTGGGGAGTTTCTGCTGAAGTCTCATCTCTCA
 GATACTACTACTTTCACGATTTGGCTGGAAACATCTTTGACTTTTGTGGTGGTG
 ATTCCTCAATGTAGGAATGTTCCCTTGTGCTGAGCTGATAGAGAAAGTATTT
 TGTGTCTCCATCCCTGTCCGAGTCAATCCGCTGGCCAGGATTTGGACGAA
 TCCTACGCCCTGATCAAGGGGCCCAAGGGATCCGACGCTGCTCTTTGCT

FIG. 5

CTGATGATGTCCTTCCTCGGCTGTTCACATCGGCCCTCCTGCTTTTCCT
CGTCATGTTTCACTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTA
AAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACTTTTGGCAAC
AGCATGATCTGCTGTTCCTAAATCACCACTCTCGGGCTGGGATGGACT
GTTGGCCCCATCCTCAACAGTGCACCTCCTGACTGTGACCCCTGATGCAA
TTCACCCCTGGAAGCTCAGTGAAGGAGACTGTGGGAACCCATCTGTGGGG
ATTTTCTTTTGTGTCAGCTACATCATATCCTTCCTGCTTGTGTGAA
CATGTACATTGCTGTCTCCTGGAGAACTTCAGCGTTGCCACAGAGAAA
GTGAGAGCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGG
GAGAACTTCGACCTGACGCCACCCAGTTTCATAGAGTTCTGCAAGCTCTC
TGACTTTGCAGCTGCCCTGGATCCTCCCTCCTCATCGCAAGCCAAACA
AAGTCCAGCTCATTTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATC
CACTGCCCTGGACATCTTATTTGCTTTTACAAAGCGGTCCTTGGGTGAG
TGGAGAGATGGATGCCCTTCGAATCCAGATGGAAGATCGGTTTCATGGCTT
CCAATCCCTCCAAGGTCTCTTATGAGCCCATTACCACCTCTGAAGGC
AAACAAGAGAGGTGTCTGCTGCTATCATCAGCGTAATTACAGATGTTA
TCTTTTAAAGCAAGGTTAAAAACATATCAAAATACGTATGACAAAGAGA
CAATCAAGGGGAGGATTTGCTTTCCTTAAAGGAGATATGGTTATTGAC
AAATTAATGGGAATTCACCCAGAAAAGACAGATGGGAGTTCTCTAC
CACCTCCCCTCCTTCTATGACAGTGTACAAAAACAGATAAGGAAAAAGT
TTGAGAAAGACAAACAGAAAAAGAAAGCAAGGGAAGAGAGGTCTGA

FIG. 5

SEQ ID NO:2

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKPKKEQDIDDENKPK
 PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLPYYVSKKTFVVLNKGKAIF
 RFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILTNCVFMTL SNP
 PDWTKNVEYTFGTGIYTFESLIKILARGFCLEDFTLRDPWNWLD FSVIVM
 AYVTEFVDLGNVSALRTFRVLRAKLTISVIPGLKTIVGALIQSVKKLSDV
 MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD
 SNGTFVNVTMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
 ICVKAGRNPNYGYTSFDTFSWAFLSLFRMLMTQDYWENLYQLTLRAAGKTY
 MIFFVLVIFLGSFYLVNLI LAVVAMAYEEQNQATLEEAQKEAEFQQMLE
 QLKQEQEEAQAVAAAASRDFSGIGGIGELLESSSEASKLSKSAKEWR
 NRRKKRQREHLEGNHRPEGRFPKSESDSVKRRSFLFSLDGNPLSGDK
 KLCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
 FEDSESRDLSLFVPHRPGERRNSVQASMSSRMVPGLPANGKMHSTVDC
 NGVSLGTTTETETEVKRRRLSSYQISMEMLEDSSGRQRAMSIASILTNTME
 ELEESRQKCPPCWYRFANVFLIWDCCDSWLKVKHIVNLI VMDPFVDLAI T
 ICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGTGIFTAEMVLKIIAMD PY
 YYFQEGWNIFDGIIVSLIMEIGLANVEGLSVLRSFRLLRVFKLAKSWPT
 LNMLIKIIGNSVGALNLTIVLAIIVFIFAVVGMQLFGKSYKECVCKINE
 DCKLPRWMNDFFHSFLIVFRVLCGEWIETMWDCEVAGQTMCLIVFMLV
 MVI GNLVVLNLFALLSSFSDDLAAATDDDNEMNNLQIAVGRMQKGIDY
 VKNKIRECFRKAFFRKPVIIEHGNKIDSCMSNNTGVVEISKELNYLKD
 GNGTSGVGTGSSVEKYVIDENDYMSFINNPSTVTVPIAVGESDFENLN
 TEEFSSESELEESKEKLNATSSSEGSTVDVAPPREGEQAEIEPEEDLKPE
 ACFTEGCIKKFPFCQVSTEEGKGKIWMNLRKTCYSIVEHNNWFETFI VFM I
 LLSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQT
 YFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRLRPLRAL S
 RFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVN
 MTTGSMFDMSEVNNFSDCQALGKQARWKNVKVNFDNVGAGYLALLQVATF

FIG. 5

KGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGV
IIDNFNQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPKQKPIPRPANKFQ
GMVDFVTRQVFDISIMILICLNMVMTMVEITDDQSKYMTLVLSRINLVFI
VLFTGEFLLKLLISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS
PTLFRVIRLARIGRILRLIKGAKGIRTLFALMMSLPALFNI GLLFLVM
FIYAIFGMSNFAYVKEAGIDDMFNFEFTFGNSMICLFQITTSAGWDGLLA
PILNSAPPD CDPAIHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVNMY
IAVILENFSVA TEESAEP LSEDDFEMFYEVWEKFDPDATQFIEFCKLSDF
AAALDPPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGE
MDALRIQMEDRFMASNP SKVSYEPIITTLKRKQEEVSAAI IQRNYRCYLL
KQRLKNI SN TYDKETIKGRIVLP IKGDMVIDKLN GNSTPEKTDGSSSTIS
PPSYDSVT KPDKEKFEKDKPEKESKGKEV

SEQ ID NO:3

TGAAAAGATGGCCCGAGCACTGCTGGTA CCCC CGGACCTGAGAGCTTCC
GCCTTTTCACTCGAGAACTCTTGTCTGCTATCGAAAAGCGTGTGCAGAA
GAGAAAGCCCAAGAA CCAAGAAAGAACAGACATTGACGATGAGAACAA
GCCAAAGCCAAACAGTGACTTGGAAGCTGGGAAGAACCTTCCATTATCT
ATGGAGACATTCTCCAGAGATGGTGTGGAGCCCTCGGAGGACCTGGAC
CCCTACTAGTCAGTAAGAAAAC TTTTGTAGTGTGAATAAAGGGAAGGC
AATTTTTCGATT CAGTGCCACCTCCGCTTGTATATTTTAACTCCACTAA
ACCCGTTAGGAAAATTGCTATTAAAGATTTGGTACACTCTTTATTTCAGC
ATGCTTATCATGTGCATATTTTACCACACTGTGTATTATGACATTGAG
CAATCCTCCTGACTGGACGAAGATGTAGAGTACACATTCACTGGGATCT
ATACCTTTGAGTCATTATAAGATCTTGGCCAGAGGATTTCTGCTTAGAA
GATTTCACAATTTCTCGTGACCCATGGAACCTGGCTGGATTT CAGTGT CAT
CGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGC
TGAGAACGTT CAGAGTTCTCCGAGCATTGAAAACAATATCAGTCATTCCA
GGTTTAAAGACCATCGTGGGGGCCCTGATCCAGTCGGTGAAGAAGCTGTC

FIG. 5

TGACGTCATGATACTCACTGTGTTCTGTCTGAGCGTCTTTGGCTCTCATCG
GGGTGCAGCTCTTCAATGGCAACCTGAGGAATAAATGCTTGCACTGGCCT
CCAAGCGATTCTGCTTTTGAGATCAACACTACTTCCACTTCAATGGCAC
AATGGACTCAATGGGACATTTGTTAATGTAA CAATGAGCACATTCAACT
GGAGGACTAATCGCAGATGACAGCCACTTTTATGTTTGGATGGACAA
AAAGATCCTTTACTTTGTGGAATGGTCCGATGCAGGACAAATGTCCAGA
AGGTTACATCTGTGTGAAGGTGGACGAAACCCCAACTACGGTTACACGA
GCTTTGACACATTTAGCTGGCCTTCTTATCGCTGTTTCGACTCATGACT
CAAGACTACTGGGAGAACCTTACCAGTTGACATTACGTGCAGCTGGGAA
AACTACATGATCTTTTTCGTCTGTGTAATTTCTTTGGCTCATTTTATT
TGGTGAACTTTGATCTCTGGCTGTGGTGGCCATGGCCCTATGAGGAA CAAAT
CAGGCCACACTGGAGGAGGCTGAGCAGAAAGAGGCGGAGTTTCAGCAGAT
GTTGGAGCAGTTGAAAAGCAGCAAGAGGAGGCTCAGGCGGTGGCAGCTG
CCTCAGCAGCGTCCAGAGACTTCAGTGGGATAGGAGGTTAGGAGAACTT
CTGGAGAGTTCTTCAGAAAGCTTCCAAGTTGAGCTCCAAGAGTGCCAAGGA
GTGGAGGAATCGAGGAAAGAAAGAGGAGACAGAGGGAGCACTTGGAGGAA
ACCACAGACCCGAAGGAGACAGGTTTCCCAAGTCGGAATCAGAAGACAGC
GTCAAGCGAAGGAGTTTCTGTTCTCCCTGGATGGGAAACCCGCTGAGCGG
CGACAAGAAGCTGTGCTCTCCCATCAGTCTCTCTTGTGATATCCGTGGCT
CCCTGTTTCCCAAGACGCAATAGCAAAACGAGCAATTTTCAGCTTCAGA
GGTCGGCGAAGGACGTGGGTCTGAGAAATGACTTTGCGGATGATGAACA
CAGCACCTTTGAAGATAGCAGAGCAGGAGAGACTCACTGTTTGTGCCGC
ACAGACCTGGAGAGCGCAACAGTAACGTTAGTCAGGCCAGTATGTCA
TCCAGGATGGTGCCAGGGCTTCCAGCCAATGGGAAGATGCACAGCACTGT
GGATTGCAATGGTGTGGTTTCTTGGGTACCACCACTGAAACAGAACTCA
GGAAGAGAAAGCTAAGTTCTTACCAGATCTCGATGGAAATGCTGGAGAT
TCTCTGGGAGACAAAGAGCCATGAGCATAGCCAGTATCTTGACCAACAC
GATGGAGGAACCTTGAAGAACTTAGACAGAAGTGTCCACCATGCTGGTATA
GATTTGCCAATGTGTTTTTGATCTGGGACTGTTGTGAATCATGGTTGAAA
GTAAAGCATCTTGTGAATTTGATTTGTGATGGATCCATTTGTTGACCTGGC
CATCACCATCTGTCATCGTTTAAACACACTGTTTCATGGCCATGGAGCACT
ATCCCGATGACGAGCAGTTTCAGCAGTGTGCTGACGGTGGGAAACCTGGTC
TTCACCGGGATCTTCACAGCGGAGATGGTCTGAAATCATCGCAATGGA
TCCCTATTACTATTTCCAGAGGGCTGGAATATCTTTGATGGAATTAATG

FIG. 5

TTAGCCTGAGTTTAATGGAGCTTGGCCCTGGCAACCGTGGAGGGGCTGTCC
 GTGCTTCGGTCTCTCAGACTGCTCGAGTCTTCAAGTTGGCAAAATCCTG
 GCCACACTGAATATGCTCATTAAGATCATCGGCAACTCGGTGGGCAC
 TGGGCAACCTGACCCCTGGTGTGCCATCATCGTCTTCATTTTGGCGTG
 GTCGGCATGACAGTGTTTGGAAAGAGCTACAAGGAGTGTGTTCAGAT
 CAATGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACT
 CCTTCTGTAGTGTTCGGGTGCTGTGTGGGAGTGGATAGAGACCATG
 TGGGACTGCATGGAGGTCCGGGCCAGACCATGTGCCTTATTGTGTAT
 GTTGGTCATGGTGATTTGGAACTTGTGTGTCTGAACCTTCTCTGGCCT
 TATTGTGAGTTCCTTTAGTTCAGACAACTTGTGCTACGGACGATGAT
 AACGAAATGAACAACCTCCAGATCGCGTGGGAAGGATGCAAAAGGGAT
 TGATTAATGTGAAAAATAAGATACGGGAGTGTCTCCGAAAAAGCGTTTAA
 GAAAGCCGAAAGTGTAGAAATCCACGAAGGAAACAAAATAGACAGTGC
 ATGTCCAATTAACACGGCGTAGTTGAAATAAGCAAGAGCTTAACACCT
 TAAAGACGGTAACGGAAACACACAGTGGGTGGGTACTGGAAGCAGTGTGG
 AGAAATACGTAATGTGATAAAATGACTACATGTCAITCATCAACAAACCC
 AGCCTCACCGTGAACGTGCCAATTTGCCGTGGGAGAGTCTGACTTTGAAAA
 TTTAAACACGGAAGAGTTTAGCAGTGAATCAGAACTGGAAGAAAGCAAGG
 AGAAATTAATGCAACCCAGCTCTTCTGAAGGAAGCACAGTTGACGTTGCT
 CCGCCCCGGAAGGTGAACAAGCTGAATGAACCTGAGGAGGACCTTAA
 GCCAGAAGCTTGCTTTACTGAAGGATGCATTAATAAATTTCCCTTCTGCC
 AAGTAAGTACGGAAGAGGTAAAGGAAATACTGGTGAATCTTAGGAAG
 ACCTGCTATAGCATTTGCGAACACAACCTGGTTTGAGACGTTTCTTGTGTT
 CATGATTTCTCTCAGTAGTGTGCTTTGGCCCTTTGAAGATATATACATTG
 AGCAACGGAAGACCATCAAAACCATGCTGGAGTATGCTGACAAAGTCTTC
 ACTTACATCTTCACTCGGAAATGCTCCTCAAATGGGTGGCCATGGATT
 TCAAAACCTAATTCACCAATGCCGTGGTGGTTGGACTTCTTGATTGTTG
 ATGTTTCTTTGGTTAGCCTGGTGGCCAAACGCTCTTGGCTATTACAGAACTT
 GGTGCCATCAAAATCCCTACGGAACCTGAGAGCTCTGAGGCCGCTCCGAGC
 CTTATCCCGCTTTGAAGCATGAGGTTGGTTGTGAACGCTCTTGTGTGGTG
 CAATCCCTCCATCATGAATGTGCTACTGGTGTGCCCTCATCTCTGTGTTA
 ATCTTTAGTATCATGGGTGTGAATCTGTTTGTGTTGTTGTTGTTGTTGTTG
 TGTTAACATGACAAACGGGAGCATGTTGACATGAGTGAAGTCAACAATT
 TCAGCGACTGTGAGGCTCTTGGCAAGCAAGCCCGATGGAAGAAATGTGAAA

FIG. 5

GTCAA CTTTGGACAA TGTGGGGCTGGCTACCTGGCA TTGCTGCAAGTGGC
CACATTCAAAGGCTGGATGGATATATGTATG CAGCTGTGGATTACGGG
ACGTCAAAC TGCAGCCTGTATATGAAGAAAATCTGTACATGTATCTGTAC
TTTGT CATCTTCATCATCTTTGGTCTCTTCACTCTAAATCTATTCTAT
CGGCGTCATCATAGACAACCTTCAAC CAGCAGAGAGAAAGTTTGGAGGTC
AAGACATCTTTATGACAGAGAGCAGRAAAAAGTACTACAATGCAATGAAG
AAACTTGGCTCCAAAAACCTCAGAGGCCATCCCTCGACCTGC AAAACA
ATTTCAAGGAATGGTCTTGACTTTGTAA C CAGACAAGTGTTTGACATCA
GCATCATGATTCCTCATCTGCCCTCAACATGGTGACCATGATGGTGGAACG
GACGAC CAGAGCAAATACATGACCTGGTTTTGTCCCGAATCAACCTGGT
ATTTCATCGTCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATCTCTCTCA
GATACTACTACTTCAGGATGGCTGGAA CATCTTTGACTTTTGTGGTGGTG
ATTCTCTCAATGTAGGAATGTTCTTGTCTGAGCTGATAGAGAAAGTATTT
TGTGTCTCCPACCTGTTC CCGAGTCA TCCGCTGGCAGGATGGACGAA
TCCTACGCTGATCAAAGCGCCAAAGGGATCCGCACGCTGCTCTTTGCT
CTGATGATGTCCTTCCCTGGCTGTTCAA CATCGGCTCCTGCTTTTCCT
CGTCATGTTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCCTATGTTA
AAAAAGAGCTGGAATTTGATGACATGTTCAA CTTTGAGACTTTTGGCAAC
AGCATGATCTGCTGTTC AAAATCACCACCTCTCGGGCTGGGATGGACT
GTTGGCCCCCATCTCAA CAGTGCACTCTGACTGTGACCTGATGCAA
TTCACCTGGAAGCTCAGTGAAGGAGACTGTGGGAACCCATCTGTGGGG
ATTTTCTTTTGTGCTAGCTACATCATATCTTCTCTGTTGTGGTGAA
CATGTACATTGCTGCTCCTGGAGAACTTCAGCGTTGCCACAGAGAAA
GTGCAGAGCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTC TGG
GAGAAGTTGACCCCTGAGCCCA CCGAGTTCTATAGAGTTCTGCAAGCTCTC
TGACTTTGAGCTGCCCTGGATCCTCCCTCCTCATCGCAAGCCAAACA
AAGTCCAGCTCATTTGCATGGACCTGCCCATGGTGAGTGGAGCCGCATC
CACTGCCCTGGACATCTTATTTGCTTTTACAAAGCGGTCCTGGGTGAGAG
TGGAGAGATGGATGCCCTTCGAATCCAGATGGAAGATCGGTTCTATGGCTT
CCAAATCCCTCCAAGTCTCTTATGAGCCCATTACCACCACTCTGAAGCGC
AAACAAGAGAGGTTGCTGTGCTATCATTCAGCGTAAATTACAGATGTTA
TCTTTTAAAGCAAAGTTAAAAACAATATCAATACGTATGACAAAGAGA
CAATCAAGGGGAGGATGTCTTGCCTATAAAAGGAGATATGGTTATTGAC
AAATTAATGGGAATTCACCCCAAGAAAAAGACAGATGGGAGTTCTCTCTAC

FIG. 5

CCTTTACTCTGTGGAAATGGCTCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTC
 GAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGGGCTTTCCCTGTCTCTATTTTCGACTCAT
 GACTCAAGACTAATGGGAAAATCTTTTACCAGTTGACATTACGTGCTGTGGGAAAACAATACATGATATTT
 TTTGTCTGTGTCATTTTCTTGGGCTCATTTTATTTTGGTGAATTTGATCCTGTGGCTGTGTGGCCATGGCCT
 ATGAGGAGCAGAAATCAGGCCACCTTGGAAAGACAGAACAAAAGAGGCCGAATTTACAGCAGATGCTCGA
 ACAGCTTAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTTCAGT
 GGAGTAGGTGGTTAGGAGAGCTGTGGAAAGTTCTTCAGAAGCATCAAGTTGAGTTCCAAAGGTGCTA
 AAGAATGGAGGAACCGGAGGGAAGAAAAGACAGAGAGAGACCTTGAAGGAAAACAACAAAGGAGAGAG
 AGACAGCTTTCCAAATCCGAATCTGAAGACAGCGCTCAAAAGAACAGCTTCCCTTTCCATGGATGGA
 AACAGCTGACCCAGTGACAAAATTTCTGCTCCCTCATCAGTCTCTCTTTGAGTATCCGTGGCTCCCTGT
 TTTCCCAAGACGCAATAGCAAAAACAAGCAATTTTCAGTTTTCAGAGGTCGGGCAAGGATGTTGGATCTGA
 AATGACTTTTGTGATGATGAACACAGCACATTTGAAGACGCGAAAGCAGGAGAGACTCAGCTGTTTGTG
 CCGCACAGACATGGAGAGCGACGCAACAGTAAAGTTAGTCAGGCCAGTATGTTCATCCAGGATGGTGCCAG
 GGCTTCCAGCAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCTTGGTGGTGGACC
 TTTAGCTTAACGTCACTACTGGAACAATTTCCCCACAGAGGCACCACTGAAACGGAAAGTCAGAAAG
 AGAAGTTAAGCTCTTACAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCAAGAGCCGTGA
 GCATAGCCAGCAATCTGACCAACACAAATGGAAGAACTTGAAGAACTAGACAGAAATGTCCGCCATGCTG
 GTATAGATTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCAATGTTAAAGTAAACATCTTTGTG
 AATTTAAATGTTATGGATCCAATTTGTGATCTTGCCATCACTATTTGCATTTCTTAAATACCCCTCTTTA
 TGGCCATGGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTTGACTGTAGGAAAACCTGGTCTTTTAC
 TGGGATTTTACAGCAGAAAATGGTTCTCAAGATCATTCAGATGGATCCTTTATTAATACTATTTCCAAGAGGC
 TGGAAATATCTTTGATGGAAATTAATGTGAGCCCTCAGTTTAAATGGAGCTTGGTCTGTCAATGTGGAGGAT
 TGTCTGTACTGGGATCATTCAGACTGCTTAGAGTTTTCAGTTGGCAAAATCCTGGCCCACTAAATAT
 GCTAATTAAGATCAATTGGCAATTTCTGTGGGGCTTAGGAAACCTCACCTTGGTGTGGCCATCATCGTC
 TTCAATTTTGTGTGGTGGCATGCAGCTCTTTGGTAAGAGCTACAAAGAAATGTGTCTGCAAGATCAATG
 ATGACTGTACGCTCCACGCTGGCAGATGAACGACTTCTTCCACTCCTTCCCTGATTTGTTCGCGTGCT
 GTGTGAGAGTGGATPAGAGACCATGTGGGACTGTATGGAGTGCCTGGCCAAACCATGTGCCCTTATTTGT
 TTCAATTTGGTTCATGGTTCATTGGAAAACCTTGTGGTCTGAACCTCTTTCTGGCCTTATTAATTGATTCAT
 TTAGCTCAGACAACTTGTGCTACTGATGACAAATGAATGAATAATCTGCAGATTCAGTAGGAAG
 AATGCAAAAGGGAATTGATTAATGTGAAAATAAGATGCGGAGTGTTCCAAAAAGCCCTTTTGTAGAAAG
 CCAAAAGTTATAGAAATCCATGAAGGCAATAAGATAGACAGCTGCATGCCAATAATACCTGGAATTGAAA
 TAAGCAAAAGAGCTTAATATCTTAGAGATGGGAATGGAAACCAAGTGGTGTAGGTACTGGAAAGCAGTGT
 TGAAAATAACGTAATCGATGAAAATGATTAATGTCAATTAATAACCAACCCAGCCCTCACCGTCACAGTG
 CCAATGTCTGTGGAGAGTCTGACTTTTGAAAACCTTAAATACTGAAGAGTTTCAGCAGTGTGAGCACTAG

FIG. 5

AAGAAAGCAAAGAGAAATTAATGCAACCACTCATCTGAAGGAAGCAGATTGATGTTGTTCTACCCCG
 AGAAGGTGAACAAGCTGAACCCGGAAGAGACTTTAAACCGGAAGCTTGTTTTACTGAAGGTGT
 ATTAAAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAGGCAAGGGAAGATCTGTGGAATCTTCGAA
 AAACCTGCTACAGTATTGTTGAGCACAACTGGTTTGAGACTTTTCAATGTGTTTCATGATCCTTCTCAGTAG
 TGGTGCAATTGGCCTTTGAAGATATATACATGAAACAGCAAGAGACTATCAAAACCATGCTAGAAATATGCT
 GACAAAGTCTTTTACCTATATATTCAATCTGGAATGCTTCTCAATGGGTGCTTATGGATTTCAAAACAT
 ATTTCACTAATGCTTGGTGGCTAGATTCTTTGATCGTTGATGTTTCTTTTGGTAGCCTGGTAGCCAA
 TGTCTTGGTACTCAGAACTCGGTGCCATCAAATCAITACGGACATTAAGAGCTTTAAGACCTCTAAGA
 GCCTATCCCGTTGAAGGCATGAGGTGTTGTAATGCTCTTGTGGAGCAATCCCTCTATCATGA
 ATGTGCTGTTGGTCTGTCTCAATCTTCTGTTGATCTTTAGCATCATGGGTGTAATTTGTTGCTGGCAA
 GTTCTACCACTGTGTTAAATGACAAACGGGTAAACATGTTTGACATTAGTGATGTTAAACAATTTAGTGAC
 TGTTCAGGCTCTTTGGCAAGCAAGCTCGGTGGAAAAACGTAAGTAACCTTTGATAATGTTGGCGCTGGCT
 ATCTTGCACTGCTCAAGTGGCCACATTTAAAGGCTGGATGGATATTAATGATGCAGCTGTTGATTACAG
 AGATGTTAAACCTCAGCTGTATATGAAGAAAACTGTACATGTAATTTATACCTTTGTTCATCTTTTATCATC
 TTTGGGTCAATCTTCACTCTGAATCTATTCAATGTTGTTGTCATCATAGATAAATTTCAACAGCAGAAAAAGA
 AGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAATATTACAATGCAATGAAGAAACTTGG
 ATCCAAGAAACCTCAGAAACCCATACCTCGCCAGCAAAACAAATTCGAAGAAATGCTCTTTGATTTGTATA
 ACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCTCAACATGGTCACCATGATGGTGGAAA
 CGGATGACCAAGGCAATACATGACCTAGTTTGTCCCGGATCAACCTAGTGTTCATTTGTTCTGTTAC
 TGGAGAAATTTGTGCTGAAGCTGGTTCCCTCAGACACTACTACTTCACTATAGGCTGGAACATCTTTGAC
 TTTGTGGTGGTGAATCTCTCCATGTAGGTATGTTTCTGGCTGAGATGATAGAAAAAGTATTCTGTGTCCTC
 CTACCTTGTTCGAGTGTATCCGTCTTGCAGGATTTGGCGAATCTACGTCTGATCAAAAGGAGCAAGGG
 GATCCGCAAGCTGCTCTTTGCTTTGATGATGTCCTTCTCGCTGTTGTTAAACATCGGCTCTCTGCTTTC
 CTGGTCAATGTTTATCTATGCCATCTTTGGGATGTCCTTCTGCTGTTGCTTAAAGGAAGCTGGAAATG
 ATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCTTGTTCCTTCCAAATTAACACCTCTGCTGG
 CTGGGATGGATTGCTAGCACCTATTCTTAATAGTGCAACCCGACTGTGACCTTGACACAATTCACCTT
 GGCAGCTCAGTTAAGGAGAGCGTGGGACCATCTGTGGGATTTCTTTTGTGAGTTACATCATCA
 TATCTCTTCTGGTGTGTGAACATGATACATCGCGGTGATCTCGAGAACTTTCAGTGTGCTACTGAAGA
 AAGTGAGAGCCCTGAGTGGATGACTTTGAGATGTTCTATGAGTTTGGGAAAAGTTTGTATCCCGAT
 GCGACCCAGTTTATAGAGTTCTCTAAACCTCTGATTTTGACAGTGCCTGGATCCCTCTTCTCTCATAG
 CAAAAACCAACAAAGTCCAGCTTATGGCATGGATCTGCCCATGGTCAGTGGTACCGGATCCACTGTCT
 TGATATTTTATTTGCTTTTACAAAGCGTGTGTTGTGAGAGTGGAGATGGATGCCCTTCGAATACAG
 ATGGAAGACAGGTTTATGGCATCAACCCCTCCAAAGTCTTATGAGCTTATTACAAACCACTTTTGAAC
 GTAAACAAGAGGAGGTGTCTGCCGCTATCATTCAGCGTAATTTAGATGTTATCTTTTAAAGCAAGGTTT

FIG. 5

AAAAAATATATCAAGTAACTATATAAAGAGGCAATTAAAGGAGGATTGACTTACCTATATAAAACAAGAC
 ATGATTTATTTGACAAACTAAATGGGAACTCCACTCCAGAAAAAAGATGGAGTTTCCCTACCAACCCCTC
 CTCCTTCCCTATGATAGTGTAAACAAAACAGAACGAAAGTTTGAGAAAGACAAACCAAGAAAAAGAAAG
 CAAAGGAAAAAGAGTCAGAGAAAATCAAAAGTAAAAAGAAAACAAAGAAATATCTTTGTGATCAATTTGTTT
 ACAGCTATGAAGGTAAAGTATATGTGTCACTGGACCTTCAAGAGGAGGTCATGCCAAAACCTGACTGTTT
 TAACAAATACCTCATAGTCAGTGCCTATACAAGACAGTGAAGTGACCTCTCTGTCACTGCAACTCTGTGAA
 GCAGGTATCAACGTTGACAAGAGGTTGCTGTTTTTATTTACCAGCTGACACTGCTGAGGAGAAAAACCAAT
 GGCTACCTAGACTATAGGGATAGTTGTGCAAAAGTGAAACATTTGTAACCTACCAAAACACCTTTAGTACAGT
 CCTTGCATCCATTCATTTTAACTTCCATATCTGCCATATTTTACAAAATTTGTTCTAGTGCATTTCC
 ATGTTCCCAATTCATAGTTTATTCATAATGCTATGTCACTATTTTGTAAATGAGGTTTACGTTGAAGA
 AACAGTATACAAGAACCTGTCTCAATGATCAGAACAGGTGTTTGGCCAGAGAGATAAAATTTTGTG
 CTCAAAACCAAGAAAAAGAAATGTAATGGCTACAGTTTCAGTTACTTCCATTTTCTAGATGGCTTTAAATTT
 TGAAGTATTTAGTCTGTGTTATGTTTGTCTATCTGAACAGTTATGTGCTGTAAGTCTCTCTCTAAATA
 TTTTAAAGGATTTATTTATGCAAAAGTATTTCTGTTTCAGCAAGTGCAAAATTTATTTCTAAAGTTTCAGAGCT
 CTATATTTAAATTTAGTCAAAATGCTTTCCAAAAGTAATCTAATAATCCATCTAGAAAAATATATCTA
 AAGTATGCTTTAGAAATAGTTGTTCCACTTTCTGCTGCAGTATGCTTTGGCATCTTCTGCTCTCAGCAA
 AGCTGATAGTCTATGTCAATTAATAACCTATGTTATGTAATAGTTATTTTATCCTGTGGTGCATGTTT
 GGGCAATATATATAGCCTGTATAACAACCTTCTATTAATCAAAATATGACCACAGTATATGTGTCTT
 TTGCAAGCTTCCAAACAGGATGTATCCTGTATCATTTCAATCAATCCATCTTCAAGCTTGGTTAAAGAAATGTCA
 TGTTAATATTTGCCATGCTGCTCTATTTTACTCAATCCATCTTCAAGCTTGGTTAAAGAAATGTCA
 ATATTGGTGATAGAAATTCACCTGCTGCTCCATTAATGCAAGCAGAAATAATTTGAAGCTATTTTAC
 AAACACTTTTACTTTTCACTTTTAAATCAACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAA
 CACACTGGATCTGCTACTGACAAAACCTATTTCTTCAATTTTGTCTAAATAATGTCTAAAAACCTTGT
 AAATATAAATAATGTAAATAATAATAATCACTTTATTTGTGTCAGCATTTTGTACATAAGAAAATTTTCA
 GGTGATGACATCACAATTTATTTTACTTTTGTCTTTGCTTTTGTATTTTAAATCAAAATCCAACTTT
 TGAATCCATAAGATTTTCAATGGATAATTTCCAAAAATAAAGTTAGATAATGGGTTTATGGATTTCT
 TTGTTATAATATATTTTCTACCAATTCAAATAGGAGATACATTTGGTCAAACTCAACCTAGATCATTTT
 CTACCACTATGTTGGCTCAATAAACCCTTTTATTCATAGATGTTTTTTTTTTTATTTTCACTTTTGTAGTA
 TTTACGTATGACACTAGTCTTTATTTTTTAAATCCTGCTGCACATAAGCTATTAACAATATAACATGGA
 CTTTGTCTTTTTTGGCATGAACAAAGTGGCAAGTTGTGCAATTAACCTAACATGATATAAATTTTTTGT
 TTTTGCACAAACCAAAAGTTTAAATGTTAAATCTTTTACAAAATATTTTACTGTAGTGTATGAAGAACT
 GCATGAGGGAAATGCTATTTGCTAAAAAGAAATGGTGAGCTACGTCATTTATTTGAGCCAAAAGAAATAAATTT
 CATTTTATTTGCAATTCACTTATTTGGGCTCTGGGGTTTTTTTTTTTTTTTTTTTTTTTTGCTGTGGCAGTTTA
 AAATATATATAATTAATAAAACCTGTGCTTGTGATCTGACATTTGTGTATACATAAAAGTTTACATGAATTTTA

FIG. 5

CAACAACTAGTGATGATTCACCAAGCAGTACTACAGAACAAAGGCAAAATAAAAGCAGCTTTGTGAAC
TTTTATGTGTGCAAGGATCAAGTTCAATGTTCCAACTTTCAGGTTTGATAATAAGTAGTAACCAACC
TACAATAGCTTCAATTTCAATTAACTCCCTTGGCTATAAGCATCAAACTCATCTCTTCAATATAAT
TGATGCTATCTCCTAATTACTTGGTGGCTAATAATGTTACATCTTTGTTACTTAAATGCATTATATAA
ACTCCTATGTATACATAAGGTATTAAATGATATAGTTATTGAGAAATTATATTAACTTTTTTCAAGAAC
CCTTGGATTTATGTGAGGTCAAAACCAAACTCTTATTCTCAGTCGAAAACTCCAGTTGTAATGCATATTT
TTAAAGACAAATTTGGATCTAAATAATGATTTTCAATAATCTCCATAATAAATTATATATAAGGTGAAAAA
AAAAAAAAAAAAAAAAAAAA

SEQ ID NO:5

GenBank® GI No.:19923381; Ref. No.:NP_008853.2; sodium channel, voltage-gated, type III, alpha; sodium channel, voltage-gated, type III, alpha polypeptide [Homo sapiens]

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKPKKEQDNDENKPKPNSDLEAGKNLPFIYDIPP
EMVSEPLEDLDPYYINKKTFIVMNGKAI FRFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILT
NCVFWTISNPPDWTKNVEYFTGIYTFESLIKILARGFCLEDFLRDPWNWLDPSVIVMAYVTEFVDLG
NVSALRFRVLRAKLTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLOW
PPSDSAFETNTTISYFNGTMDSNGTFVNVMTSTFNWKDYIGDDSHFYVLDGQKDPLLCNGSGDAGQCPEGY
ICVKAGRNPNYGYTSFDTFSWAFSLFRMLTQDVWENLYQLTLRAAGKTYMIFVIVIFLGSFYLVNLIL
AVVAMAYEEQNQATLEAEQKEAEFQQMLEQLKKQEEAQAVAAASAAASRD FSGVGLGELLESSSEASK
LSKGAKEWRNRKRQRREHLEGNNGERDSFPKSESEDSVKRSSFLFSMDGNRLTSDKKFCSPHQSLL
SIRGSLFSPRRNSKTSIFSFRGRADVGSNDFADEHSTFEDGESRRDSLFPVPHRHGERNSNVSQASM
SSRWVPGIPANGKMHSTVDCNGVVSIVGGPSALTPTGQLPPEGTTTETETVRKRLSSYQISMEMLDSS
GRQAVSTASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVXHLVNLIVMDPFVDLAITICI
VLNTLFWAMEHYPMTEQFSSVLTGVNLVFTGIFTAEMVLKIITIGNSVGALGNLTFLAIIIVFIFAVVGMQLFGKSYKE
LSNVEGSLVLSRFLRLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTFLAIIIVFIFAVVGMQLFGKSYKE
CVCKINDDCTLPRWHMNDFFHSFLIVFRVLGGEWLETWDCMEVAGOTMCLIVFMLVMVIGNLVVLNLF
ALLLSFSSDNLAAATDDDNEMNLIQIAGVRMQGIDYVKNMRECQKAFRRKPKVIEIHEGNKIDSCMS
NNTGIELSKELNLRDNGTTSVGTGSSVEKYVIDENDYMSFINNPSTVTVPIAVGESDPENLNTEEF
SSESELEESKEKLNATSSSEGSTVDVVI.PREGQAETEPEEDFKPEACFTGCIKKFPFCQVSTEEGKGK

FIG. 5

IWNLRKTCVSIVEHNWFETIVFMILSSGALAFEDIVIEQRKTIKTMLEYADKVFTYIFILEMLLKWV
AYGFQTYFTNAWCWLDLIVDVSLVSLVANALGYSELGAIKSLRTRALRPLRALSRFEGMRVVVNALVG
AIPSIMNVLLVCLIFWLIFSIMGVNLFAKFPYHCVMNMTGNMFDISDVNNLSDCOALGKQARWKNVKVNF
DNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIFGSSFTLNLFIGVIIDN
FNQKKKFGGQDIFWTEEQKXYNAMKKLGSKKPQPIPRPANKFQGMVDFVTFQVFDISIMILICLNM
VTMMVETDDQKYMVLVSRINLVFIVLFTGEFVLKLVSLRHYFTIGWNIFDFVVVILSIVGMFLAEMI
EKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLFALMMSLPALFNIGLLFLVMFIYAIFGMSNFAYV
KKEAGIDDMFNFTFGNSMICLFQITTSAGWDGLLAPILNSAPPCDDPTIHPGSSVKGDRGDPVGIFF
FVSYIIISFLVVVNMYTAVILENFSVATEESAEPLEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAAL
DPPLLIAKPNKQOLIAMDLPVMVSGDRJHCLDILFAFTKRVLCESGEMDALRIQMEDRFMASNPFSKVSYPE
ITTTILKRKQBEVSAIIIQNFRCYLLKQRLKNISSNYNKEAIKGRIDLPIKQDMIIDKLNNGNSTPEKTDG
SSSTTPPPSYDSVTKPKDKKFEKDKPEKESKGKEVRENQK

SEQ ID NO:6

GenBank® GI No.: 12642271; GB No.:AF225986.1; Homo sapiens voltage-gated sodium channel alpha subunit splice variant SCN3A-s (SCN3A) mRNA, complete cds, alternatively spliced

AGCGAAGCGGAGGCATAAGCAGAGAGGATTCGGAAAGGTCTCTTGTGTTTTCTTATCCACAGAGAAAGAA
AGAAAAAAATGTAACTAATTTGTAAACCTCTGTGCTCAAAAAAAGCTGAAACAGC
TGCCAGAGGAAGACACGTTATACCCTAACCATCTTGGATGCTGGGCTTTGTTATGCTGTAATTCATAAGG
CTCTGTTTTATCAGAGATTATGGAGCAAGAAAACTGAAGCCCAAGCACATCAAGGTTTGACAGGGATGAG
ATACCTGTCAAGGATTCATAGTAGTGGCTTACGGGAAAGGAGCAAGAAATCTCTTAGGGATATTG
TAAGATAAATGAGATAATTACAGAGAGGACCTGGAGCTTTCCGGAAAAAGGTGCTGTGACTATCTAA
GGTAATTCGTATGCAAGAAGCTACACGTAATTAATGTGCAGGATGAAAAGATGGCACAGGCACTGTTGG
TACCCCGAGGACCTGAAAGCTTCGCTTTTACTAGAGAACTCTTGTCTGCTATCGAAAAACGTGCTGC
AGAAGAGAAAGCCAAAGAGCCCAAGAGGAAACAAGATAATGATGATGAGAACAAACCAAGCCAAATAGT
GACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGACATCTCCAGAGATGGTGTGAGAGCCCC
TGGAGGACCTGGATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAGGAAAGGCAATTTT
CCGATTCAGTGCCACCTCTGCCTTGATATATTTTAACTCACTAAACCCTGTTAGGAAAAATTGCTATCAAG

FIG. 5

ATTGTTGGTACATTTCTTTATTACAGCATGCTTATCATGTGCACTATTATTGACCAACTGTGTATTATTATGACCT
 TGAGCAACCCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACCTGGAATCTATACCTTTTGAGTCACAT
 TATAAAAATCTTGGCAAGAGGGTTTTCCTTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTG
 GATTTTCAGTGTCAATTGTGATGGCAATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTTGAGAA
 CATTCAGAGTTCTCCGAGCCTGAAAAACAATTTTCAGTCATTCAGGTTTAAAGACCAATGTGGGGGCCCT
 GATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATCCTGACGTGTCTGTCTGAGCGGTGTTTGTCTCTC
 ATTGGGCTGCAGCTGTTTCATGGCAATCTGAGGAATAAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTT
 TTGAAACCAACACACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTTGTAAATGTAAACAAT
 GAGCACATTTAACTGGAAAGGATTAATTTGGAGATGACAGTCACATTTTATGTTTGGATGGGCAAAAAGAC
 CCTTTACTCTGTGGAAATGGCTCAGATGCAGGCCAGTGTCCAGAAAGGATFACATCTGTGTGAAGGCTGGTC
 GAAACCCCAACTATGGCTACACAAGCTTTTGACACCTTTTAGCTGGGCTTTCCTGTCTCTATTTTCGACTCAT
 GACTCAAGACTATTTGGGAAAATCTTTTACCAGTTGACATTCAGTGTGCTGTGGGAAAAACATACATGATATTT
 TTTGTCTGCTGTTCAATTTCTTGGCTCAATTTTATTTGGTGAATTTGATCCTGGCTGTGGTGGCCATGGCCT
 ATGAGGAGCAGAAATCAGGCCACTTGGAAAGCAGAACAAAAAGAGGCCGAATTTTCAGCAGATGCTCGA
 ACAGCTTAAAGCAACAGGAAGACTCAGGCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTTCAGT
 GGAGTAGGTGGTTTAGGAGAGCTGTTGGAAAGTTCTTCAGAAAGCATCAAAGTTGAGTTCCAAAGGTGCTA
 AAGATGGAGGACCGGAGGAGAAAGAACAGACAGAGAGAGCACCTTGAAGGAAACAACAAGGAGAGAG
 AGACAGCTTTCCAAATCCGAATCTGAAGACAGCGTCAAAAGAGCAGTTTCTTTTCTCCATGGATGGA
 AACAGACTGACAGTGCACAAAAAATCTGTCCCTCATCAGTCTCTCTTGAGTATCCGTGGCTCCCTGT
 TTTCCCAAGACGCAATAGCAAAAACAAGCATTTTTCAGTTTCAGAGGTGCGGCAAGGATGTTGGATCTGA
 AAATGACTTTTGTGTGATGAAACACAGCAATTTTGAAGACAGCGAAAGCAGGAGAGACTCACTGTTTGTG
 CCGCACAGACATGGAGAGCGACGCAACAGTAAACGGCACCACTGAAACGGAAAGTCAGAAAGAGAAAGGT
 TAAGCTCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAAGGCAAGAGCCGTGAGCATAGC
 CAGCATTCAGCAACACAAATGGAAGAACTTGAAGAACTTAGACAGAAATGTCCGCCATGCTGGTATAGA
 TTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGATGGTTAAAGTAAACAATCTTGTGAATTTAA
 TTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTGTCATTGCTTAAATACCCCTTTTATGGCCAT
 GGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTGACTGTAGGAAACCTGGTCTTTTACTGGGAT
 TTTCACAGCAGAAATGGTTCTCAAGATCAATGCCATGGATCCTTATTAATATTCCAGAAAGGCTGGAATA
 TCTTTGATGGAAATATTGTTCAGCCTCAGTTTAAATGGAGCTTGGTCTGTCAAATGTGGAGGGATGTCTGT
 ACTGGCATCAATTCAGACTGCTTAGAGTTTTCAGTTGGCAAAATCCTGGCCCCACACTAAATATGCTAAAT
 AAGATCAATGGCAATCTGTGGGGCTCTAGGAAACCTCACCTTGGTGTGGCCATCATCGTCTTCATTT
 TTGCTGTGGTCGGCATGCAGCTCTTTGGTAAAGAGCTACAAAGAAATGTGTCTGCAAGATCAATGATGACTG
 TAGCTCCACGGTGGCACATGAACGACTTCTTCCACTCTTCTGATTTGTTCCGCGTGTGTGTGGA
 GAGTGGATAGAGACCATGTGGGACTGTATGGAGGTGCTGGCCAAACCATGTGCCCTATTGTTTTCATGT

FIG. 5

TGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTTCTGGCCCTATTATTAGATTCAATTTAGCTC
 AGACAAACCTTGTGCTACTGTAGATGACAAATGAATGAATAATCTGCAGATTGCAGTAGGAAGAATGCAA
 AAGGGAATTGATTATGTGAAAAATAAGATCGGGAGTGTTCAAAAAGCCTTTTTAGAAAAGCCAAAAG
 TTATAGAAAATCCATGAAGGCAATAAGATAGACAGCTGCATGTCCAAATAATACCTGGAATGAAATAGCAA
 AGAGCTTAATTATCTTAGAGATGGGAATGGAACCAACCAAGTGGTGTAGGTACTGGAAGCAGTGTGGAAAA
 TACGTAATCGATGAAAAATGATTTATATATGTCAATTCATAACCAACCCAGCCTCACCGTCACAGTGCCTAATTG
 CTGTTGGAGAGTCTGACTTTGAAAACTTAATACCTGAAGAGTTCAGCAGTGAATGATGTTGTTCTACCCCGAGAAGGT
 CAAAGAGAAAATTAATGCAACCAAGCTCATCTGAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGT
 GAACAAGCTGAAACTGAACCCGAAGAAGACTTTAAACCCGAAGCTTGTCTTACTGAAGGTGTATTAAAA
 AGTTCCATTTCTGTCAAGTAAGTA CAGAAGAAGGCAAGGGAAGATCTGGTGGAACTTTCGAAAAACCTG
 CTACAGATTGTTGTAGCA CAACCTGGTTTGAGACTTTCAATGTGTTCATGATCCTTCTCAGTAGTGGTCA
 TTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAAACCAATGCTAGAAATATGCTGACAAAG
 TCTTTACCTATATATTCATTTCTGGAATGCTTCTCAATGGGTGCTTATGGATTTCAAAACATATTTTAC
 TAATGCTGTTGCTGGCTAGATTTCTTGATCGTTGATGTTCTTTGTTAGCCTGGTAGCCAATGCTCTT
 GGTACTCAGAACTCGGTGCCATCAATCAATACGGACATTAAGAGCTTTAAGACCTTAAGAGCCTTAT
 CCCGGTTTGAAGCATGAGGGTGGTTGTGAATGCTCTTGTGGAGCAATCCCTCTATCATGAATGTCT
 GTTGGTCTGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTGTGGCAAGTTCTAC
 CACTGTGTTAACATGACAAACGGGTAAACATGTTTGACATTAGTGATGTTAAACAATTTGAGTGA CTGTGAGG
 CTCTTGGCAAGCAAGCTCGGTGGAAAAACCTGAAGTAAACTTTGATAATGTTGGCGTGGCTATCTTGC
 ACTGCTTCAAGTGGCCACATTTAAAGGCTGGATGGATATATGATGACAGCTGTTGATTCACGAGATGTT
 AAATTCAGCCTGTATATGAAGAAAATCTGTACATGATTTATATCTTTGTCTATCATCTTTTGGGT
 CAATCTTCACTGTGAATCTATTCAATGTTGTCTCATVAGATAA CTTCACACGACAGAAAAAGAAAGTTGG
 AGGTCAAGACATCTTTTATGACAGAGGAACAGAAAAAATATTACAATGCAATGAAGAAACTTTGGATCCAAG
 AAACCTCAGAAACCCATACCTCGCCAGCAAA CAAATTCAGGAATGGTCTTTGATTTTGTAAACAGAC
 AAGTCTTTGATATCAGCATCATGATCCTCATCTGCCCTCAACATGGTCAACATGATGGTGGAAACGGATGA
 CCAGGGCAATACATGACCCCTAGTTTGTCCCGGATCAACCTAGTGTTCATTTGTTCTGTTCACCTGGAGAA
 TTTGTGCTGAAGCTCGTTTCCCTCAGACACTACTTCACTATAGCTGGAAACATCTTTGACTTTGTGG
 TGGTGATTTCTCTCCATTTGATAGGTATGTTTCTGGCTGAGATAGAAAAATATTCTGTCTCCCTACCTTT
 GTTCCGAGATGATCCGTCTTGGCAGGATTTGGCCGAATCCATCGTCTGATCAAGAGCAAGGAGATCCGC
 ACGTGTCTTTTGTCTTTGATGATGTCCCTTCTCTGCGTTGTTTAAACATCGGCCCTCTCTCTCTTCTGTTCA
 TGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGCCCTATGTTTAAAAAGGAAGCTGGAAATGATGACAT
 GTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGTGTTGTTCCAAATTAACAACCTGTGCTGGCTGGAT
 GGAATGTAGACCTATTCTTAATAGTGACCAACCCGACTGTGACCTGTGACACAAATTCACCCCTGGCAGCT
 CAGTTAAGGAGACCGTGGGACCCATCTGTGTTGGGATTTCTTTTGTGTCAGTTACATCATCATATCTCTT

FIG. 5

CCTGGTTGTGTGAACATGTACATCGGGTTCATCTCGGAACTTCAGTGTTCCTACTGAAGAAAGTGCAGAGCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAAAGTTTGATCCCGATCGGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGAGCTGGCTGGATCCTCTCTTCATAGCAAAACC
 CAACAAAGTCCAGCTTATGCGCATGGATCTGCCCATGGTCAGTGGTGACCGGATCCACTGTCTTGATATT
 TTTATTTGCCCTTACAAAGCGTGTGTTGTGTGAGAGTGGAGAGATGGATGCCCTTCGAAATACAGATGGAAG
 ACAGGTTTATGGCATCAACCCCTCCAAAGTCTCTTATGAGCCTATTACAAACCACTTTGAAACGTAAACA
 AGAGGAGGTGTCTGCCGCTATCATTCAGCGTAAATTTTCAGATGTTATCTTTTAAAGCAAGGTTAAAAAAT
 ATATCAAGTAACTATAACAAAGAGGCAATTAAGGGAGGATGACTTACCTATAAACAGACATGATTA
 TTGACAAACTAAATGGGAACCTCCACTCCAGAAAAACAGATGGGAGTTCTCTACCACTCTCCTCCTTC
 CTTATGATAGTGTAAACAAACAGACAAGGAAAGTTTGGAGAAAGACAAACAGAAAAAGAAAGCAAGGA
 AAAGAGGTCAAGAAAAATCAAAAGTAAACAAAGAAATCTTTGTGTGATCAATTTGTTTACAGCCT
 ATGAAGGTAAAGTATATGTGTCAACTGGACTTCAAGAGGAGGTCCATGCCAAACTGACTGTGTTTAAACAAA
 TACTCATAGTCAGTGCCTATACAAAGACAGTGAAGTGAACCTCTCTGTCTCACTGCAACTCTGTGAAGCAGGGT
 ATCAACGTTGACAAAGAGGTGCTGTTTATACAGCTGACACACTGCTGAGGAGAAACCAATGGCTACC
 TAGACTATAGGATAGTTGTGCAAAAGTGAACATTTGTAACCTACACCAACACACTTTAGTACAGTCTCTGCA
 TCCATTTCTATTTTAACTTCCATATCTGCCATATTTTACAAAATTTGTCTAGTGCATTTCCATGGTCC
 CCAATTCATAGTTTATTCATTAATGCTATGTCATATTTTGTAAATGAGGTTTACGTTGAAGAAACAGTA
 TACAAGAACCCCTGCTCTCAAAATGATCAGACAAAGGTGTTTGGCCAGAGAGATAAAATTTTGTCTCAAAA
 CCAGAAAAAGAAATGTAATGGCTACAGTTTCAGTTACTTCCATTTCTAGATGGCTTTAAATTTTGAAGT
 ATTTTAGTCTGTATGTTTGTCTATCTGAACAGTTATGTGCTGTAAAGTCTCCTCTAAATATTTAAAG
 GATATATTTTATGCAAAAGTATCTGTTTTCAGCAAGTGCAAAATTTTATTTCTAAAGTTTCAGAGCTCTATATT
 TTAATTTAGGTCAAAATGCTTTCCAAAAAGTAACTTAATAATCCATCTAGAAAAAATATATCTAAAGTATT
 GCTTTAGAAATAGTTGTTCCACTTTCTGCTGCAGTATTTGCTTTGCCATCTTCTGCTCTCAGCAAAAGCTGAT
 AGTCTATGTCAATTAAATACCTATGTTTATGTAATAATAGTATATTTTATCCTGTGGTGCATGTTTGGGCAAA
 TATATATATAGCCTGATAAACAACTTCTATTAATCAAAATGTAACCAAGTATGTATGTTCTTTTGCAG
 CTTCCAACAGGATGATCCTGTATCATTCATTAACATAGTTTAAAGGCTATCACTAATGCAATGTTAAT
 ATGGCTATGCTGCTCTATTTTACTCAATCCATTTCTCAAGTCTTGGTTAAAGATGTCACATATTGG
 TGATAGAAATGAATCAACCTGCTCTGCCATTAATGTCAGCAGAAATAATTTGAAGCTATTACAAACACC
 TTTTACTTTTGGCACTTTTAAATCAACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAAACACACTG
 GATACCTGCTACTGACAAACCTATTCTTCATATTTTGTCTGCAATTTGTACATAAGAAATAATTTTTCAGGTTGAT
 AATAATGTAAAAATAATAACAACTTTTATTTGTGCAATTTTGTACATAAGAAATAATTTTTCAGGTTGAT
 GACATCACAATTTATTTTACTTTTATGCTTTTGTGATTTTAAATCAAAATTTCCAAACCTTTTGAATCC
 ATAAAGATTTTCAATGGATAATTTCTTAAATAAAGTTAGATAATGGGTTTTATGGATTTCTTTGTTAT
 AATATATTTTCTACCATTCCAATAGGAGATACATTTGGTCAACACTCAAAACCTAGATCATTTTCTACCAA

FIG. 5

CTATGGTGCCTCAATATAACCTTTTATTCAATGATGTTTTTTTATTCAACTTTTGTAGTATTACGT
 ATGCAGACTAGTCTTTATTCTTTTAAATCTCTGCTGCACATAAGCTATTACAAATATAACATGGACTTTGT
 CTTTTAGCCATGAACAAAGTGGCAAGTTGCGCAATTACCTAACATGATATAAAATTTTTGTTTTGCA
 CAAACCAAAAGTTTAAATCTTTTACAAAACATTACTGTAGTATTTGAAGAACTGCATGCA
 GGAATTCGTATTGCTAAAGAAATGGTGAAGTACGTCAATATTGAGCCAAAAGATAAATTCATTTT
 TATTGCATTTCACTTATTGGCTCTGGGTTTTTTGTTTTTTGTTTTGCTGTGGCAGTTTAAATATA
 TATAATTAATAAACTGTGCTTGATCTGACATTTGATACATAAAAGTTTACATGAATTTTACAACAAA
 CTAGCGCATGATTCACCAAGCAGTACTACAGAAACAAAGGCAATTAAGCAGCTTTGTGAACCTTTTATG
 TGTGCAAGGATCAAGTTCAATGTTCCAACTTTCAGGTTTGATATAATAATAGTAGTAACACCTACATA
 GCTTCAATTTCAATTAACTCCCTTGGCTATAAGCATCTAAACTCATCTTCTTCAATATAATGATGCT
 ATCTCCTAATTACTTGGTGGCTAATAAATGTTACATTTCTTTGTTACTTAAATGCATTATATAAATCCTTA
 TGATACATAAGGTATTAATGATATAGTTAATGAGAAATTTATATACTTTTTTTTCAAGAACCTTTGGA
 TTTATGTGAGGTCAAAACCAACTCTTATCTCAGTGGAAACTCCAGTTGTAATGCATATTTTAAAGA
 CAATTTGGATCTAAATATGTTATTCATAATTCCTCCATAATAAATATATAAGGTGGAAAAA
 AAAAAAAAAA

SEQ ID NO:7

GenBank® GI No.:12642272; GB No:AAK00218.1; AF225986_1 voltage-gated sodium channel alpha subunit splice variant SCN3A-s
 [Homo sapiens]

MAQALLVPPGPESFRLFTRSLAAIEKRAAEKAKPKKKEQDNDENKPKNSDLEAGKNLPFIYGDIPP
 EMVSEPLEDLDPYINKKTFIVMNGKAIFFSATSYLTPLNPVRKIAIKILVHSLFMSLMCTILT
 NCVFMTLSNPPDWTKNVEYFTGIYTFESLIKILARGFCLIEDFTFLRDPWNWLDPSVIVMAYVTFVDLG
 NVSALRTRFVLRALKTISVIPGLKTIVGALIQSVKLSVDMILTVFCLSVFALIIGLQFMGNLRNKLQW
 PPSDAFETNTSYFNGTMDNSGTFVNVMTSTFNWKDYIGDDSHFYVLDGQKDPLLCNGSDAGQPEGY
 ICVKAGRPNPYGTSFDTFSWAFSLFLRLMTQDYNLYQLTLRAAGKTYMIFVLVFLGFSFYLVNLIIL
 AVVAMAYEEQATLEAAEQKEAEFQOMLEQLKKQEEAAQVAAASASRDFSQVGLGELLESEASK
 LSSKGAKWRNRKRRQRREHLEGNNGKGRDSFPKSESDSVKRSFLFSDMGNRLTSDKKFCSHQSL
 SIRGSLFSPRNSKTSIFSFRGAKDVGSENDFADDEHSTFEDSESRDLSLFVPHRGERRNSNGTTTET
 EVRKRRLSSYQISMEMLEDSGRQRAVSTASILTNTMEELESQRKPCPCWYRFANVFLIWDCCDAWLKV

FIG. 5

AAGCGTCTGAGAAAGAAAGCCAAAGAAACCCAAAGAAAGAGCAAGACATTGACGATGAGAAACAAACCA
 AAGCCAAACAGCGACTTGAAGCTGGGAAGAAACCTTCCATTATCTATGAGAGACATTCTCTCCAGAGATGG
 TGTGAGAGCCCTGGAGGACCTGGACCCCTACTATGTGCTAGTAAGAAACCTTTGTAGTGTGAATAAAGG
 GAAGCGATTTTTCGATTGAGTTGAGTTCAGCGCCACCTCCGCCCTGTATATTTAACTCCGCTAAACCTGTTAGGAAA
 ATTGCCATTAAAGATTTTGGTACACTCTTTGTTGAGCATGCTTATCATGTGCATATTTTGACCAACTGTG
 TATTTATGACGTTGAGTAATCCTCCCGACTGGACAAAGATGTAGAGTATACGTTCACTGGGATCTATAC
 CTTTGAGTCACTTATATAAGATCTTTGGCAAGAGGTTTTCCTTAGAAGATTTCACTTTCTCCGTGACCCCA
 TGGAACTGGCTGGATTTGAGTGTGATCGTGTGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCT
 CAGCGCTGAGAACCTTTCAGAGTTCTCCGAGCATTGAAACAAATATCAGTCATTCAGGTTTAAAGACCAT
 CGTGGGGCCCTGATCCAGTCCGTGAAGAGCTGCCGACGTATGATCCTCACCGTGTCTGTCTCAGT
 GTCTTTGCTCTAATCGGGCTGCAGCTCTTCAATGGGCAACCTGAGGAATAAATGCTCGCAGTGGCCCCCGA
 GCGATTCGGCTTTTGAACCAACACTACTTCTCTACTTCAATGGCACAAATGGATTCAAATGGGACATTTGT
 TAATGTAACAATGAGCACTTTCAACTGGAAGGATATATCGCAGATGACAGTCACTTTTATGTCTTTGGAT
 GGACAAAAGATCCTTTTACTCTGTGGAAATGGCTCCGATGCAGGACAAATGTCAGAGGTTACATCTGTG
 TGAAGGCTGGACGAAACCCCACTACGGCTACACAAGCTTTTGACACCTTCAGCTGGGCCCTTTGTCCCT
 GTTTCGACTCATGACTCAGGACTTACGGGAGATCTTTACAGTTGACATTCGCTGCGTGGGAAACC
 TACATGATATTTTTCGTCTGTGTAATTTCTTTGGGCTCGTTTATTTGGTGAACCTTGATCCTGGCTGTGG
 TGGCATGGCCCTATGAGGAGCAGAACCCAGGCCACACTGGAGAGGCTGAAACAGAAAGGACAGAGTTTCA
 GCAGATGCTGGAGCAACTGAAGAGCAGCAGGAGGAGGCTCAGGCATGGCTGCAGCCTCCGCGGCATCC
 AGAGACTTCAGTGAATAGGAGGTTAGGAGAACTTCTGGAGAGTTCTTCAGAGCTTCCAAAGTTGAGCT
 CCAAGAGTGTAAAGGAGTGGAGAACCGGAGGAAGAGAGAGACAGAGGGAACACTTGGAGGGAAACCA
 CAGAGCGGATGGAGACAGGTTTCCCAAGTCGGAATCGGAAGACAGTGTCAAACGAAGAAGCTTCTCTGCTC
 TCCCTGGATGGCAACCCGCTGACTGGTGACAAAGAGCTGTGCTCTCCCAACAGTCTCTCTTGAGTATCC
 GTGGCTCCCTGTTTTCCCAAGACGCAATAGCAAAACGAGCAATTTTCAGCTTCAGAGGTCGGCGGAAGGA
 CGTGGGGTCTGAGATGACTTTGCAGACGATGAGCACAGCACTTCGAGSACAGCGAGAGCAGGAGAGAC
 TCCCTGTTTGTGCCGACAGACCTGGAGAGCGACGCAACAGTAAACGTTACCACTGAAACCGGAAGTCA
 GGAAGAGAAGGCTAAGTTCTTACAGATTTCAATGAAATGCTGGAGGATTCCTCTGGAAGACAAAGATC
 CATGAGCATAGCCAGTATCCTGACCAACACCATGGAGGAACCTGAAGAACTAGACAGAGTGGCCACCA
 TGTCTGATATAGTTCCCAATGTGTTTTTGTCTGGGACTGTGTGATGATGATGTTAAAGTGAAGCATC
 TTTGGAATTTAATGTGATGGATCCATTTGTGTGATCTTGGCATTAACAAATTTGTCATCGTATTAATACACT
 GTTTCATGGCCATGGAGCATATCCCATGACCCAGCAGTTTCAGCAGTGTGTGACTGTGGGAAACCTGTGTC
 TTTCACTGGGATCTTCACAGCCGAAATGGTCTCTTAAATCATTTGCCATGGACCCCTATTATTATTTTCCAAAG
 AGGGCTGGAAATTTTTCGATGGAATTTATTTAGCTGAGTTTAAATGGAGCTAGGCCCTGGCAAAATGTGGA
 GGGGCTGTCTGTGCTTCGGTCTTCAGACTGCTCCGAGTCTTCAAGTTGGCAAAAGTCTCTGGCCCCACACTG

FIG. 5

TTTTCTGGTCACTTTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCATATGTTAAAAAGAGGCTGG
 AATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGCATGATCTGCTGTTTCCAATCACCACCTCT
 GCCGCTGGACGGACTGCTGGCCCCCATCTCAACAGCGCACCTCCGACTGTGACCCCGATGCAATTC
 ACCCTGGAAGCTCGGTGAAGGGGACTGTGGAAACCCATCCGTGGGATTTCTTTTGTCAAGCTACAT
 CATATATCTTCTCGTGGTGGTGAACATGTACATCGCTGTCTCTGGAGAACTTCAGCGTCGCCACC
 GAAGAAAGTGCAGAGCCCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAAGTTTCGACC
 CTGACGCCACTCAGTTTCATAGAGTTCTGCAAGCTTTCGACTTTTGCAGCTGCCCTGGATCTTCCCTCCT
 CATCGCAAGCCCAACAAAGTCCAGCTCATTTGCCATGGACCTGCCATGGTGGAGTGAGACCGCATCCAC
 TGCCTGGACATCTTGTCTTGTCTTTTACAAGCGGTCTTGGCGAGAGTGGAGAGATGGACGCTCTTCGAA
 TCCAGATGGAAGATCGCTTCATGGCTTCCAAACCCCTCCAAAGTCTCTTATGAGCCCATTTACCACCCCT
 GAAACGGAAACAAGAGGAGGTGCTGCTGCTATCATTCAGCGTAATTATAGATGTTATCTTTTAAAGCAA
 CGGTTAAAAACAATATCGAGTAAATAACGACAAGAGACAATCAAGGGAAGGATTTGACTTGGCTATATAAG
 GAGATATGGTTATTGACAAATTTGAATGGGAATTCACCCAGAAAAGACGGATGGGAGTTCTTCCACAAC
 CTCTCTCTCTTCCATGACAGTGTAAACAAACAGATAAGGAAAAGTTTGAGAAAGACAAACCAAGAAAA
 GAAATCAAGGGGAAGAGGTCAAGAGAAATCAAAAGTAAAAAGAGACAAAGAAATGTCTTTGTAATCAAT
 TGTTTACAGCCCTCTGAAGGTAAAGTATCCGTCTCAACTGGAATTAAGGAGAGGTCCATGCCAAACTGAC
 TGTTCACAAATACTCAAGGTCAAGTGCCTATATACAGACAGTGACCTCTGTCACTGCCACTCTGTGAGAC
 AGGTATCAACATTTGACAAGAGGTGCTGCTTCCATTACAGCTGACACTGTCTGAGGAGAACTCCATTGT
 GCAAGTGACCCGTCATCATGCCCCCAACTCCCATTAGTACAAAGTCTCTGTCTCATCTATTTTAAACATCA
 CATTTGCCATATTTTACAAAACTGTCCCAGTGTATCTTCTGTTCCCACTTCATAGTCTGTTCATAA
 TACTATGTCACATATTTTGTAAATGAAGTTTACGTTAAGGAAAAATATATATATAAGAAATCCCATGTTGC
 TAAGTCCACAAGTTTCTCCAGTAATCATAAAAAATAATTTTGCTGAGAGATGAAATTTATGCTCAAAAC
 AAAAAAAATAAATCTAAATGTTAACAGTTTC

FIG. 5

SEQ ID NO:9

GenBank® GI No.:6981510; Ref. No.:NP_037251.1; sodium channel, voltage-gated, type III, alpha polypeptide [Rattus norvegicus]

MAQALLVPPGESFRLFTRESLAAIEKRAAEKAKPKKEQIDDDENKPKNSDLEAGKNLPFIYGDIPP
 EMVSEPLEDLDPYVVKKTFVVLNKGKAI FRFSATSALYILTPINPVRKIAKILVHSLFMSLMIMCTILT
 NCVFMTLSNPDPWTKNVEYFTFTGIYTFESLIKILARGFCLEDFTFLRDPNNWLD FSVIMAYVTFVDLG
 NVSALRTFRVLRAKLTISVIPGLKTI V GALIQSVKLSVMILTVFCLSVFALIGLQLFMGNLRNKCQW
 PPSDAFETNTTSYFNGTMD SNGTFVNVTMTSFNWKDYIADDSHFYVLDGQDPLICGNGSDAGQCPEGY
 ICVAGRNPNGYTSFDTFSWAFSLFRLMTQDYWENLYQLTLRAAGKTYMIFVVLVFLGSFYLVNLIL
 AVVAMAYEEQNQATLEEAQKEAEFQQMLEQLKKQEEAQAVAAAASARDFSGIGLGELLESSSEASK
 LSSKSAKEWRNRKRRQREHLEGNHRADGRFPKSESDSVKRRSFLLSLDGNPLTGDKKLCSPHQSLL
 SIRGSLFSPRRNSKTSIFSFRGRKADVGSENDFADDSHSTFDESRRDSL FVPHRPGERRNSNGTTTET
 EVRKRLSSYQISMEMLEDSSGRQSRMSIASILTNTMEELEESRQCPWCYRFANVFLIWDCCDAMLKV
 KHLVNLIVMDPFVDLAITICIVILNTLFMAMEHYPMTQQFSVLT VGNLVTGIFTAEMLVKI IAMDPIYY
 FQEGWNI FDGIIIVSLMELGLANVEGLSVLRSFRLRVFKLAKSWPTLNMLIKIIIGNSVGALGNLTIVL
 AIIIVFAVGMQLFGKSYKECVCKINVDCKLPRWHMNDFFHSFLIVFRVLCGEWETMWD CMEVAGQTM
 CLIVFVMLVMVIGNIVNLFLALLSSFSNDNLAATDDDNEMNNLQIAVGRMQGIDFVKNKIRECFRKA
 FFRKPKVIEIQEGNKIDSCMSNNTGIEISKELNYLKDNGTTSVGVTGSSVEKYVIDENDYMSFINNPSL
 TVTVPIAVGESDFENLT EEFSESELEESKEKLNATSSSEGSTVDVAPREGGEQAEIPEEDLKPEACF
 TEGCIKKFPFCQVSTEEGKGIWNNLRTCYSI VEHNWFETFI VFMILLSSGALAFEDIYIEQRKTIKTM
 LEYADKVFTYIFILEMLLKWVAYGFQYFTNACWLD FLIVDVSLVSLVANALGYSELGAIKSLRILRAL
 RPLRALSRFEGNRVVNALVGAIPSI MNVLIVCLIFWLIFSI MGVLNLFAGKFYHCVTNTTGNMFEIKEVN
 NFSDCQALGKQARWKNVKNFDNVGAGYLALI QVATFKGWM D IMYAAVDSRDVKLQPI YEENLYMYLYFV
 IFIIFGSFFITLNLFIGVI IDNPNQKKKFGGQDIFWTEQKKKYNNAMKKLGSKKPQKPI PRPANKFQGMV
 FDFVTRQVFDISIMILICLNMVTMMVETDQSKYMTLVLSRINLVFIVLFTGEFLIKLISIRYYFTIGW
 NTFDFVVILSIGVMFLAELEK YFVSPITLFRVIRLARIGRILRLIKAGAKGIRTLIFALMMSLPALFNIG
 LLLFLVMFIVAI FGMSNFAYVKEAGIDDMFNFTFGNSMICLFQITTSAGWDGLLAPILNSAPDCDDPD
 A IHPGSSVKDCGNPSVGIFEFVSYIIISFLVVNNMYIAVILENFSVATEESAEPIS EDDFEMFVEWKEK
 FDDATQFIEFKCLSDFAALDPPILLIAENKVQLIAMDLPMVSGDRHICLDILFAFTKRVLGESGEMDA
 LRIQMEDRFMASNP SKVSEYPTITTLKRQEEVSAALIQRNRYCYLLKQRLKNISSKYDKETIKGRIDLIP
 IKGDMVIDKLNGNSTPEKTDGSSSTTSPPSYDSVT KPDKEKFEKKEIKGKEVRENQK

FIG. 5

SEQ ID NO:10]

GenBank® GI No.:9055329; Ref. No.:NM_018732.1; Mus musculus sodium channel, voltage-gated, type III, alpha polypeptide (Scn3a), mRNA

TTTTTATATCTGTGAGTGACGAAAGAAAAAGAAAAAGAAATGCAAAATAAAAAATGTTGAG
CCCCAGTTAATGTCAGGATTTTAATCAATTCATTTGAGGAACTACTTTAAAGCATGTAGAAGC
TGAGGATAGTGGTCATATCTTAACACCAGTACTTTGGGAGGTGAAGCCAGAACTAGCCTAGATTAC
TCTCAGATATATTGTAAGTTTGAGGCTAGCCTGGGCTACATGAACCTGTATCTCATCCACACATAAAAA
AAGTTTGATATATTTGGTATATTAAACAATGATATAACAAAAGTTTGAATATATAGCAAAATAATTGG
TAAAAGTACCTACTATATATATATATATATACATATATACATATATATGTATATACATATATATAT
GTATTTTAAATTAACATAAGCTTTTAAATCGAATATCTTACCTTTTAAAGAGAAATGTAATTCA
TATTTCAACATTCCTTCAGTTTCTAGAGTAGAATCTGAAGTGACAGTTGATGCATAGTAGTGTCTGTT
GTGTGCATCTGTCTGTCAATCCATCCACGCTTTGCCACCTGTAATTAGAGACCTTTTACACAGGCAAG
GGCCCAAGGCTCTGGGAGTCTGTAAATTAAGTATTAATTTTCTTAGTCGATCTAAATGAAAAATA
AGTAAATCTAAATTAGATTTATAAAGAAAAAATGTGCTGAATAACGACTTGATTTACACCTTAATA
TTATTAACACCTTTTGTGGAATCTACATTAATGATCAACTCATAAATAATAGTCTAGCTTCCAAGTG
TACTCAATTAAGATCATCGGCAACTCGGTGGGCGCACTGGCAACCTGACCTGGTGTGTTGCAAGATCAA
ATGCTCAATTTTCCGCTGGGATGAGACCATGTGGGACTGCAATGGAGTCGGGGCCAGACCATGTGCCCTTATTG
CTGTGTGGGAGTGGATAGAGACCATGTGGGAACTTGTGGTCTGAACTTTTCTGGCTTATTGTGAGTTC
TGTTTATGTTGTCATGTTGTTGGGAACTTGTGGTCTGAACTTTTCTGGCTTATTGTGAGTTC
CTTTAGCTCAGACAACTTGTGCTACGGACGATGATAACGAAATGAACAACTCCAGATCGCGGTGGGA
AGGATGCAAAAGGGATTGATTATGTGAAAAATAAGATACGGGAGTGTCTCCGAAAGCCTTTTITAGAA
AGCCGAAAGTATAGAAATCCACGAAGGAAACAAATAGACAGCTGCATGTCCATAACACGGGCGTAGT
TGAATTAAGCAAGAGCTTAACCTTAAGACGGTAAACGAAACCAACAGTGGCGTGGGTACTTGGAGC
AGTGTGGAGAAATACGTAATTGATGAAATGACTACATGTCATTCATCAACACCCAGCTTCCAGTGA
CGGTGCCAATTTGCCGTGGGAGTCTGACTTTGAAATTTTAAACACGGAAGAGTTTAGCAGTGAATCAGA
ACTGAAGAAAGCAAGGAGGTAAAGCGCTTTTTCAGTTTCAGCCACCACTTTTGGCCTTCTACACAGTA
TGGCTCTCTGATTTGTTTTCCTGTGAGGTGCTTAATCAACAGAAAGAAATGGGTGGGTGTGTAG
CTCAAGGGATAGGATACCTTAGCATGCATGACGTCTTGTAGTACCCCAACACACCCCAAAAGCACTTA
AACCTAGATAAAGTTGGAACATCATGAGAAATGGGTAAAGTTCTGTTTAAATATACTTTCCCATAGGAAAT

FIG. 5

CACAACTTGAGCGATTAAATGTTTCATTTCTTGATAACCTGAAAGCCGATTTAATATGCAATCCTAAC
AAAAGAGATACATAATTAACACATTTTCCCTCGCTAGTTATTTGTTTATAGAAAACCTCAATGAACATAAT
TTAATGGTGGTAGCCATCACGTGTGAAAAATTTACATAGCTCTTTATTCACATTTAAGTGTTTTATTTACC
AATTTGTTTACTAGGAAGGTCAGCCATACCTGATATTTTCCCTATTAAAGATGAGCAAAACCTATGACAT
TTTCTACATTAACCTTAAATACTGAAGATTAAACATTTGATGATTTATAGTGATCTACAGATGGGAAAT
TTCCGTCAATAGTAGTTGATCGAATGAAAGAGAAAATTTTCATATGCTATGATTTGAGCTCATTTGG
GTCTAATGACAAATAGCTTAGTGACATTACCTTCAATATTTTATTTATTTATTTATGGCCTTTGGATGT
AACAGCTGGAGGTTAATCTAGCACAGATGGTGTATAAAGGATCTCTAGCTGGAGGGAATCCTCAACACC
CTGGAACAGACCATAATGTTTGTATCTATGGATTTCTCTGGAGCTTTTGAAAAACCAAGTTACACCAAGAT
AATTTGCTCTAGAAATCCTTATAGAAATTTATGGCATCAAACTCACAGTGTCCCAATCTTTTTCATAT
TTTGAATAATGTTTAAACCTAAAAACATATGAACAAAATGAGGTAGCAATGTTTATTTTACAGTTGC
ACATAATTTGTGCATAGCACATCTAATTCACGTTGCTCATCTCTAGTCTAGTAAGACTCAATCTTGGCTTTA
TTTTCTATCACCTGGCGTAGAATTGACTTACAAAGAACCTTAGAGGACTAGCAGGCATTCAGTACTAT
TTTTGTCCAAATTCGGTCAAAGACAGTCTTTATCAAGTGTGTTCCCAACAACTCATAAAGTCATTAAACTC
TATTTAATTGATCTACAGGCCGTGTTTAAATTTTAGGCGTTTAAGAAATGGGAAGGAGTTAAATGAC
AGAAATTTGTAATAGGCCCTCATATTTGGGTACATCGTTAAAAAGTGGAAAGATACCTGTTCTCCAAAGGA
GAGCAGGGTTGATAATGAGCTCTGTTTACTCAGGCGAGTGGAGAGCAGGAGACAGGCAAAAGGATGTGC
CGGTGTGTCTGGAAGCTCCAGACTGCAGCCTTGCAAGATAACTCGGAGCTTGGAAATTTCTGCAATGTTCA
CGAAGGAGTGTCTTAAACAGAAAGCAATTAGAAAGGGGTATCCTAGGAACATCTGTTTATTAAAGAGTAAA
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GCCAAAATAATAGAGAACCAAGCGTAATTGGCAATTTACAGACCTCAAGAATCTGAGGAATCAGAAAGT
GGCAATTCACCTGTCTGATAAGGGCTTCTGAGGAAGGTCAACAGGTTTGTATGAAAGGAATTC

SEQ ID NO:11

GenBank® GI No.:9055330; Ref: NP_061202.1; sodium channel, voltage-gated, type III, alpha polypeptide [Mus musculus]

MLIKIGNSVGALNLTLLVLAIIIVFIPAVVGMQLFGKSYKECVCKINEDCKLPRWHMNDFFHSFLIVFRV
LCGEWETMWDMEVAGQTMCLIVFMLVMVIGNLVNLFLALLSSFSNDLAATDDDNEMNNLQIavg
RMQKIDYVKNKIRECFRKAFFRKPKVIEIHEGNKIDSCMSNNTGVVEISKELNYLKDNGNTTSGVGTGS
SVEKXVIDENDYMSFINNPSSLIVTVPIAVGESDFENLNTTEEFSSSELEESKEVSALFSSGHHFCAIYTV
WLLCTIVFCL